



Sequence Listing

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Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kljasin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.

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Gly Tyr Tyr Lys Asn Ile His Asp Ile Ile Pro Asp Arg Ser Gly	215	225	225
Pro Glu Leu Gly Gly Asp Ala Thr Ile Arg Lys Met Leu Ser Phe	230	235	240
Trp Trp Pro Leu Ala Leu Ile Leu Ala Thr Gln Arg Ile Ser Arg	245	250	255
Pro Ile Val Asn Leu Phe Val Ser Arg Asp Leu Gly Gly Ser Ser	260	265	270
Ala Ala Thr Glu Ala Val Ala Ile Leu Thr Ala Thr Tyr Pro Val	275	280	285
Gly His Met Pro Tyr Gly Trp Leu Thr Glu Ile Arg Ala Val Tyr	290	295	300
Pro Ala Phe Asp Lys Asn Asn Pro Ser Asn Lys Leu Val Ser Thr	305	310	315
Ser Asn Thr Val Thr Ala Ala His Ile Lys Lys Phe Thr Phe Val	320	325	330
Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe Trp Thr	335	340	345
Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val Asp	350	355	360
Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser	365	370	375
Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp	380	385	390
Leu Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val	395	400	405
Leu Arg Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr	410	415	420
Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala	425	430	435
Gly Phe Val Gly Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr	440	445	450
Val Tyr Arg Lys Gln Lys Lys Lys Met Glu Asn Glu Ser Ala Thr	455	460	465
Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu	485	490	

<210> 8
<211> 535
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 66, 96, 387
<223> unknown base

<400> 8
actacagaa gtgccccga gctggggag atncaacatt aagaagatgc 50
tgaactttctg gtgccttttg gctctaatto tgccacaca gagaancagt 100
aggaactattg tcaacctett tgtttccggg gacctgggtg gcagttctgc 150
agacacagag gcagtgggca ttttgacagc cacataacct gtgggtcaca 200
tgcatacgg ctgggtgaag gaaatccgtg ctgtgtatcc tgccttcgac 250
atgataacc ccagcaacaa actgggtgag acgagcaaca cagtcacggc 300
ggacacata aagaagttaa ccttcgtctg catggtctg tcaactcagg 350
tctgttcgt gatgttttg acacccaacg tgtctgngaa aatcttgata 400
cacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttcttt 450
tcggatcttc tctttcttc cagttccagt cacagtgagg gcgcattctc 500
ccgggttggc gatgacactg aagaaaacct tcgtc 535

<210> 9
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361
<223> unknown base

<400> 9
tgaaggatc ccgggttggg tctctgggt tngacaagat aaacccccag 50
caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100
agttcacctt ngtttgnatg gntctgtcaa ctcaagctnt gtttcgtgat 150
gttttggaca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200
tggantttgc ctttgcagaa ntttgngntg ttcttttgcg gattttctcc 250
tttttccag ttccagtcac agngaggggc catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgaggatca 350
ttgtctnat ngccagcett gtggtcctac cctacctggg ggtgcacggg 400
tgacctgg gegtgggttc cctcctggcg ggca 434

<110> 10
<111> 154
<112> DNA
<113> Homo sapiens

<110>
<111> unsure
<112> 31, 49, 63, 83, 90, 98, 119
<113> unknown base

<400> 10
tattccaggt tccggtcacg gggagggcgc atntcacggg gtggctgang 50
cattgaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100
agctctatc gccagcctng ttgtcctacc ctacctgggg gtgcacgggtg 150
gat 154

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatacggg tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gtctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcattcttc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
gttccgcca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
gggaaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
acctgctgtg gtcacaggtc tccg 24

<210> 17
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
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gactgctgg gagcctgctc cctgctcagc tgcgctcct gcctctgcgg 100
ctctgcccc tgcctcctgt gcagctgtg ccccgccagc cgcaactcca 150

cogtgagccg cctcatcttc acgttcttcc tcttcoctggg ggtgctgggtg 260
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300
tcgactgttg ctccctgctt gggtaccgg ctgtctaccg catgtgcttc 350
gccacggggg ccttcttctt ctctcttttc acctgctca tctctgctt 400
gagcagcagc cgggaccccc gggtgccat ccagaatggg ttttggttct 450
ttaagttcct gatcctgggtg gggtccaccg tgggtgacct ctacatccct 500
gacggctcct tcaccaacat ctggttctac ttggcgctcg tgggtcctt 550
cctcttcacg ctcatccagc tgggtgctgt catcgacttt ggcactcct 600
ggaacccagc gtggctgggc aaggccgagg agtgccttc ccgtgcttg 650
taaggaggcc tcttcttctt cactctcttc ttctacttgc tctcgatcgc 700
ggcctggggc ctgatgttca tgaactaac tgagcccagc ggtgcccacg 750
agggcaaggt cttcatcagc ctcaacctca cctctgtgt ctggtgtcc 800
atgctgctg tctgcccac ggtccaggac gccagccca actcgggtct 850
gctgcaggcc ttggtcatca cctctaacg catgtttgt acctggtcag 900
ccctatccag tatccctgaa cagaaatgca acccccattt gccaacccag 950
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gtgggatgac ccgagcattg tgggctcat catcttcttc ctgtgcacc 1050
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cagaccagg agtgcccacc tatgctagac gccacacagc agcagcagca 1150
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gatgatcagc acgtggacg ccgtgtgggt gaagatctgt gccagctggg 1350
cagggtgtt cctctacctg tggacctg tagccccact cctcctggcg 1400
aacccgact tcagctgagg cagcctcaca gctgcacac tgggtgctcc 1450
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caccatcag ccaggctgag ccccacccc tgcaccagct ccaggacct 1550
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 ggggaactcc caccacagtg gggcctccgg cactgaagcc ctggtgttcc 1800
 ttgtcagctc ccccagggga cctgcccccc ttctgggact tegtgcctta 1850
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900
 a 1901

<210> 19

<211> 457

<212> PFT

<213> Homo sapiens

<400> 19

Met	Gly	Ala	Cys	Leu	Gly	Ala	Cys	Ser	Leu	Leu	Ser	Cys	Ala	Ser	1	5	10	15
Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Ile	Leu	Cys	Ser	Cys	Cys	Pro	20	25	30	35
Ala	Ser	Arg	Asn	Ser	Thr	Val	Ser	Arg	Leu	Ile	Phe	Thr	Phe	Phe	35	40	45	50
Leu	Phe	Leu	Gly	Val	Leu	Val	Ser	Ile	Ile	Met	Leu	Ser	Pro	Gly	55	60	65	70
Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly	75	80	85	90
Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser	95	100	105	110
Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	115	120	125	130
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	135	140	145	150
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	155	160	165	170
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr	175	180	185	190
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val	195	200	205	210
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	215	220	225	230

Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu	135	190	195
Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr	200	205	210
Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe	215	220	225
Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe	230	235	240
Ile Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala	245	250	255
Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu	260	265	270
Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser	275	280	285
Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro	290	295	300
Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr	305	310	315
Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile	320	325	330
Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His	335	340	345
Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met	350	355	360
Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu	365	370	375
Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr	380	385	390
Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met	395	400	405
Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met	410	415	420
Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp	425	430	435
Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu	440	445	450
Leu Arg Asn Arg Asp Phe Ser	455		

<117> 20
<118> 24
<119> DNA
<120> Artificial Sequence

<121>
<122> Synthetic oligonucleotide probe

<123> 24
gggagctcat cttaacgttc ttaa 24

<124> 21
<125> 29
<126> DNA
<127> Artificial Sequence

<128>
<129> Synthetic oligonucleotide probe

<130> 21
cctatcagct ggtgctgctc 20

<131> 21
<132> 29
<133> DNA
<134> Artificial Sequence

<135>
<136> Synthetic oligonucleotide probe

<137> 22
ctctttccac ttctgcctgg 20

<138> 23
<139> 18
<140> DNA
<141> Artificial Sequence

<142>
<143> Synthetic oligonucleotide probe

<144> 23
cctggggcaaaa aatgcaac 18

<145> 24
<146> 24
<147> DNA
<148> Artificial Sequence

<149>
<150> Synthetic oligonucleotide probe

<151> 24
caggaatgta gaaggcaccc acgg 24

<152> 25
<153> 24

<217> DNA
<218> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 25
tgcacacagat ctccacccac acgg 24

<210> 25
<211> 50
21. DNA
<218> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 25
tgtccatcat tatgtgagc cggggcgtgg agagtcagct ctacaagctg 50

<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
gagcagaggc ggggaactgaa ggtgtgggtg tcgagccctc tggcagaggg 50
ttaaactggg tcaaatgcac ggattctcac ctcgtaacgt taagttctcc 100
cgcggaactg ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150
aggtcgagag aaggccatgg aggtgcgcgc accggcaccg cggagcttcc 200
ctgttagagc attgtgccta tttcccccag tttttgctgc cgaagctgtg 250
actgcgcatt ccgaagtcct tgaggagcgt cagaagcggc ttccctacgt 300
cccagagccc tattacccgg aatctggatg ggaacgcctc cgggagctgt 350
ttggcaaaag tgaacagcag agaatttcaa aggaacttgc taatatctgt 400
aagaacgcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450
agctttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500
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cgaggcttca ttcgttatgg ctggcgctgg ggttggagaa ctgcagtgtt 600
tgtgaactata ttaaacacag tgaacactag tctgaatgta taccgaaata 650
aagatgcctt aagccatttt gtaattgcag gagctgtcac ggggaagtctt 700
tttaggataa acgtaggcct gcgtggcctg gtggctgggt gcataattgg 750
agccttgcgt ggcactctgt taggaggcct gctgatggca ttccagaagt 800

cctggatga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850
 cactggttaa aactggaaga gtggaaaggc agactacaag ttactgagca 900
 cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950
 atgctaagaa aattgaagca ctgctaaacc ttcttagaaa cccttcagta 1000
 ctgataaac aagacaagga ctgaaagtgc tetgaacttg aaactcactg 1050
 gagagctgaa gggagctgcc atgtccgatg aatgccaca gacaggccac 1100
 tctttggtca gcttctgac aaatttaagt gctggtacct gtggtggcag 1150
 tgccttactc ttgtcttttt cttttctttt taactaagaa tggggctggt 1200
 ctactctcac ttactttatc cttaaattta aatacatact tatgtttgta 1250
 ttaactatc aatatatgca tacatggata tatccacca cctagatttt 1300
 aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350
 + 1351

<C10> 28
 <C11> 285
 <C12> PET
 <C13> Homo sapiens

<100> 28
 Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala
 1 5 10 15
 Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala
 20 25 30
 Asp Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val
 35 40 45
 Pro Glu Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu
 50 55 60
 Leu Phe Gly Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala
 65 70 75
 Asn Ile Cys Lys Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val
 80 85 90
 Tyr Gly Gly Ile Pro Ala Phe Ile His Ala Lys Gln Gln Tyr Ile
 95 100 105
 Glu Gln Ser Gln Ala Glu Ile Tyr His Asn Arg Phe Asp Ala Val
 110 115 120
 Gln Ser Ala His Arg Ala Ala Thr Arg Gly Phe Ile Arg Tyr Gly
 125 130 135

Trp Arg Trp Gly Trp Arg Thr Ala Val Phe Val Thr Ile Phe Asn		
	140	150
Thr Val Asn Thr Ser Leu Asn Val Tyr Arg Asn Lys Asp Ala Leu		
	155	165
Ser His Phe Val Ile Ala Gly Ala Val Thr Gly Ser Leu Phe Arg		
	170	180
Ile Asn Val Gly Leu Arg Gly Leu Val Ala Gly Gly Ile Ile Gly		
	185	195
Ala Leu Leu Gly Thr Pro Val Gly Gly Leu Leu Met Ala Phe Gln		
	200	210
Lys Tyr Ala Gly Glu Thr Val Gln Glu Arg Lys Gln Lys Asp Arg		
	215	225
Lys Ala Leu His Glu Leu Lys Leu Glu Glu Trp Lys Gly Arg Leu		
	230	240
Gln Val Thr Glu His Leu Pro Glu Lys Ile Glu Ser Ser Leu Arg		
	245	255
Glu Asp Glu Pro Glu Asn Asp Ala Lys Lys Ile Glu Ala Leu Leu		
	260	270
Asn Leu Pro Arg Asn Pro Ser Val Ile Asp Lys Gln Asp Lys Asp		
	275	285

c110: 19
 c111: 374
 c112: DNA
 c113: Homo sapiens

c400: 29
 cgggaagtcgc ttgaggagcg tcagaagcgg ctccctacg tcccagagcc 50
 ctattaccgc gaatctggat gggaccgctc cgaggagctgt ttggcaaaga 100
 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagaaggcag 150
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200
 catgctaacc aacaatacat tgagcagagc caggcagaaa tttatcataa 250
 ccgggtttgat gctgtgcaat ctgcacatcg tgetgccaca cgaggcttca 300
 ttcgttcatg gctggcgccg aacc 324

c110: 30
 c111: 377
 c112: DNA
 c113: Homo sapiens

c220:

<221> unsure
<222> 262, 330, 371
<223> unknown base

<400> 30
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accgcgqagc tttttttctgt agagcattgt gctatttcc ccgagttttt 100
gctgccqaag ctgtgactgc cgattccgaa gtccttgagg agcgtcagaa 150
ggggttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
gcctccqgga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250
cttgcctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300
gtatggqgga ataccagctt ttattcatgn taaacaacaa tacattgagc 350
agagccaggc agaaatttat nataacc 377

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
tcgtacagtt acgtctctcc 20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 32
ctctgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaataatct gtaagacggc agctacagca ggcattcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

gagcgcgcgc cgcgcgcgcgc cgcgcgcactg cagcccccagg ccccgccccc 50

ccaccacagt ctgcgttgct gcccgcctg gcccaggccc caaaggcaag 100

gacaaagcag ctgtcaggga acctcgcgcg gactcgaatt tacgtgcagc 150

tgcgcgcaac cacagggttc aagatggttt gggggggctt cgcgtgttc 200

aagaactgcc tgtgcgcct caacctgctt tacaccttg ttagtgtct 250

gctaattgga attgctgct ggggcattgg ctccgggctg attccagtc 300

tccgagtggc cggcgtggc attgcagtg gcattctctt gttcctgatt 350

gcttttagtg gtctgattg agctgtaaa catcatcagg tgttgctatt 400

tttttatatg attattctgt tacttgctt tattgttcag tttctgtat 450

cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500

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aaactgctgt gggttccgaa gtgttaacc aatgacacc tgtctggcta 600

gctgtgttaa aagtgaccac tcgtgtctgc catgtgtcc aatcatagga 650

gaatatgctg gagaggtttt gagatttggt ggtggcattg gcctgttctt 700

cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750

agaaagacc cgcgcgcaat cctagtgcct tcctttgatg agaaaacaag 800

gaagatttcc tttcgtatta tgatcttggt cactttctgt aattttctgt 850

taagctccat ttgccagttt aaggaaggaa aactatctg gaaaagtacc 900

ttattgatag tggaattata tatttttact ctatgtttct ctacatgttt 950

ttttctttcc gttgctgaaa aatatttgaa acttggtggtc tctgaagctc 1000

ggtggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050

cctttcttag catttttacc tgcagaaaaa ctttgtatgg taccactgtg 1100

ttggttatat ggtgaatctg aacgtacatc tcaactggtat aattatatgt 1150
 agcaactgtgc tgtgtagata gttcctactg gaaaaagagt ggaaatttat 1200
 taaatcaga aagtatgaga tectgttatg ttaagggaaa tccaaattcc 1250
 ctattttttt tgggtttttt aggaagatt gttgtggtta aaagtgttag 1300
 tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350
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 aggttaagtgc aaaggagaag tggtttcatg aaatgttcta atgtataata 1450
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 aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550
 aagactgcct tttaaaaca gttagtatta atgcgttggc ccagtagca 1600
 aaaagatatt tgattatctt aaaaatttgt aaataccgtt ttcatgaaat 1650
 ttctcagtat tgtaacagca acttgctaaa cctaagcata tttgaatatg 1700
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750
 cttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800
 taaaagaaag taatggaag 1819

<110> 36
 <211> 204
 <212> PFT
 <213> Homo sapiens

<400> 36
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 Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile
 20 25 30
 Ala Ala Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val
 35 40 45
 Val Gly Val Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala
 50 55 60
 Leu Val Gly Leu Ile Gly Ala Val Lys His His Gln Val Leu Leu
 65 70 75
 Phe Phe Tyr Met Ile Ile Leu Leu Leu Val Phe Ile Val Gln Phe
 80 85 90
 Ser Val Ser Cys Ala Cys Leu Ala Leu Asn Gln Glu Gln Gln Gly
 95 100 105

Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn	
				110					115					120	
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn	
				125					130					135	
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser	
				140					145					150	
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val	
				155					160					165	
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu	
				170					175					180	
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp	
				185					190					195	
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu							
				200											

<110> 37
 <111> 390
 <112> DNA
 <113> Homo sapiens

<120>
 <121> unsure
 <122> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336
 <123> unknown base

<400> 37
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 tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttggt 100
 tagccttgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200
 gttcogaagt gtttaaccba atgacacctg tntggctagc tgtgttaaaa 250
 gtgaccactn gtgctcgcca tgtgctcaa tcataggaga atatgctgga 300
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<210> 38
 <211> 566
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 27

<227> unknown base

<499> 38

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ttttgaatt ttacaggtaa gtgcaaagga gaagtggttt catgaaatgt 200
ttatgttat aataacattt accttcagcc tccatcaga atggaacgag 250
ttttaagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
tttttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350
ttggccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
ttttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450
ttatattga atatgatctc ccataatttg aaattgaaat cgtatttgtt 500
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tttgtgccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<219>

<211> unsure

<221> 84-85, 206

<223> unknown base

<400> 39

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cttatttagc cctgaaacc aggagcaaca gggnnacagt tcttgagagt 100
tgggttgcaa caatcacggc caagtgaact cgcaaatac atcccagaga 150
tactctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200
tggatngctg tgttaaaagt gacctcgt gctcgccatg tgcctcaatc 250
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<219>

<223> Synthetic oligonucleotide probe

<100> 40
ccttacgtct gcgttgctgc c 21

<110> 41
<111> 18
<112> DNA
<113> Artificial Sequence

<114>
<115> Synthetic oligonucleotide probe

<400> 41
caggaatgctg tggagagg 18

<110> 42
<111> 21
<112> DNA
<113> Artificial Sequence

<114>
<115> Synthetic oligonucleotide probe

<400> 42
caggaatgcac taggattcgc gcgg 24

<110> 43
<111> 45
<112> DNA
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<114>
<115> Synthetic oligonucleotide probe

<400> 43
gagcccaag gcaaggacaa agcagctgtc agggaaacctc cgccg 45

<110> 44
<111> 2061
<112> DNA
<113> Homo sapiens

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<210> 45
 <211> 359
 <212> PFT
 <213> Homo sapiens

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 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser
 35 40 45
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe
 50 55 60
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val
 65 70 75
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe
 80 85 90
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp
 95 100 105
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly
 110 115 120
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys
 125 130 135
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro
 140 145 150
 Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val
 155 160 165
 Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala
 170 175 180
 Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys
 185 190 195

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr
				200					205					210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe
				215					220					225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys
				230					235					240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln
				245					250					255
Leu	Gln	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro
				260					265					270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala
				275					280					285
Pro	Gln	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser
				290					295					300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro
				305					310					315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp
				320					325					330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu
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Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu	
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 47

tttcacacgc caattctc 18

<210> 48

<211> 23
<112> DNA
<113> Artificial Sequence

<210>
<215> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<112> DNA
<113> Artificial Sequence

<210>
<215> Synthetic oligonucleotide probe

<400> 49
agtttgggt gtcttcagtg gctg 24

<210> 50
<211> 45
<112> DNA
<113> Artificial Sequence

<210>
<215> Synthetic oligonucleotide probe

<400> 50
gtgagggacc tgtctgcaat gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<112> DNA
<113> Homo sapiens

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<216> 52

<211> 321

<212> P&T

<213> Homo sapiens

<400> 51

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Asp	Thr	Tyr	Gly	Arg	Pro	Ile	Leu	Glu	Val	Pro	Glu	Ser	Val	Thr
				20					25					30
Gly	Pro	Trp	Lys	Gly	Asp	Val	Asn	Leu	Pro	Cys	Thr	Tyr	Asp	Pro
				35					40					45
Leu	Gln	Gly	Tyr	Thr	Gln	Val	Leu	Val	Lys	Trp	Leu	Val	Gln	Arg
				50					55					60
Gly	Ser	Asp	Pro	Val	Thr	Ile	Phe	Leu	Arg	Asp	Ser	Ser	Gly	Asp
				65					70					75
His	Ile	Gln	Gln	Ala	Lys	Tyr	Gln	Gly	Arg	Leu	His	Val	Ser	His
				80					85					90
Lys	Val	Pro	Gly	Asp	Val	Ser	Leu	Gln	Leu	Ser	Thr	Leu	Glu	Met
				95					100					105
Asp	Asp	Arg	Ser	His	Tyr	Thr	Cys	Glu	Val	Thr	Trp	Gln	Thr	Pro
				110					115					120
Asp	Gly	Asn	Gln	Val	Val	Arg	Asp	Lys	Ile	Thr	Glu	Leu	Arg	Val
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Gln	Lys	Leu	Ser	Val	Ser	Lys	Pro	Thr	Val	Thr	Thr	Gly	Ser	Gly
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Tyr	Gly	Phe	Thr	Val	Pro	Gln	Gly	Met	Arg	Ile	Ser	Leu	Gln	Cys
				155					160					165
Gln	Ala	Arg	Gly	Ser	Pro	Pro	Ile	Ser	Tyr	Ile	Trp	Tyr	Lys	Gln
				170					175					180
Gln	Thr	Asn	Asn	Gln	Glu	Pro	Ile	Lys	Val	Ala	Thr	Leu	Ser	Thr
				185					190					195

Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe
				200					205					210
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile
			215						220					225
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys
			230						235					240
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser
			245						250					255
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr
			260						265					270
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe
			275						280					285
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr
			290						295					300
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His
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 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Synthetic oligonucleotide probe

<400> 53
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<210> 54
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<400> 54
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<210> 55
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 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Synthetic oligonucleotide probe

<10> 55

ttcacatg tgctgtgct gctc 24

<10> 56

<11> 24

<11> BHA

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<20>

<20> Synthetic oligonucleotide probe

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agcacaatcc agcagctggc ttac 24

<10> 57

<11> 56

<11> DNA

<11> Artificial Sequence

<20>

<20> Synthetic oligonucleotide probe

<100> 17

tcgptcaccg gagcaactac acgtgtgaag tcacctggca gactcctgat 50

<110> 58

<111> 2458

<112> RNA

<113> Homo sapiens

<400> 58

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185	190	195
Gln Asn Leu Thr Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr Ala	
200	205	210
Gly Asn Glu Ala Gly Lys Glu Ser Cys	Val Val Arg Val Thr Val	
215	220	225
Val Tyr Val Gln Ser Ile Gly Met Val	Ala Gly Ala Val Thr Gly	
230	235	240
Ile Val Ala Gly Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu Leu	
245	250	255
Ile Arg Arg Lys Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg Pro	
260	265	270
Asn Glu Ile Arg Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu Val	
275	280	285
Lys Pro Ser Ser Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser Gly	
290	295	300
Ser Ser Ser Thr Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser Gln	
305	310	315
Arg Thr Leu Ser Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala Thr	
320	325	330
Gln Ala Tyr Ser Leu Val Gly Pro Glu	Val Arg Gly Ser Glu Pro	
335	340	345
Lys Lys Val His His Ala Asn Leu Thr	Lys Ala Glu Thr Thr Pro	
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<223> Synthetic oligonucleotide probe

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actaggtgt atgcttgggt gggc 24

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<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

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				20					25					30	
Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	
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Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	
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Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	
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Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	
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Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	
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Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	
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Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Gln	Cys	Thr	Cys	Pro	Pro	
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Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	
				140					145					150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	
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Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	
				170					175					180	
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				185					190					195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	
				200					205					210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	
				215					220					225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	
				230					235					240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	
				245					250					255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	
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Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	
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Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His	290	295	300
Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser	305	310	315
Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly	320	325	330
Pro Lys Arg Gly His Pro Arg Gln Asn Leu His Lys His Phe Asp	335	340	345
Ile Asn Glu His Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu	350	355	360
Val Leu Val Val Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg	365	370	375
Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	380	385	390
Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	395	400	405
Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys	410	415	420
Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	425	430	435
Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	440	445	450
Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His	455	460	465
Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	470	475	480
Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg	485	490	495
Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	500	505	510
Leu Pro Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser	515	520	525
Pro Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	530	535	540
Ser Pro Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	545	550	555
Pro Leu Leu Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	560	565	570

Ser Arg Asn Gly Ser Phe Ile Thr Lys Glu Lys Lys Asp Thr Val	
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Leu Arg Gln Val Arg Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe	
590	600
Asp Asp Met Leu His Phe Leu Asn Pro Glu Glu Leu Arg Val Ile	
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Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu	
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<210> 67
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<210> 68
 <211> 2412
 <212> DNA
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<400> 68

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<211> 453

<212> FFT

<213> Homo sapiens

<400> 69

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				20					25					30

Pro	Asp	Ala	Asp	Ala	Val	Ala	Ala	Gln	Ile	Leu	Ser	Leu	Leu	Pro
				35					40					45

Leu	Lys	Phe	Phe	Pro	Ile	Ile	Val	Ile	Gly	Ile	Ile	Ala	Leu	Ile
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Leu	Ala	Leu	Ala	110	Gly	Leu	Gly	110	His	Phe	Asp	Cys	Ser	Gly
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Arg	Cys	Asp	Gly	Val	Ser	Asp	Cys	Lys	Asp	Gly	Glu	Asp	Glu	Tyr
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Val	Ser	Ser	Asp	Asn	Leu	Arg	Val	Ser	Ser	Leu	Glu	Gly	Gln	Phe
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Arg	Glu	Glu	Phe	Val	Ser	Ile	Asp	His	Leu	Leu	Pro	Asp	Asp	Lys
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Val	Thr	Ala	Leu	His	His	Ser	Val	Tyr	Val	Arg	Glu	Gly	Cys	Ala
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Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu	Glu
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Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr		
365	370	375
Gly Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr		
380	385	390
Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val		
395	400	405
Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe		
410	415	420
Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg		
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<211> 24

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<220>

<223> Synthetic oligonucleotide probe

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<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

ctacacgtccc tgtggttgca gatc 24

<210> 72

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 72

cgttcaatgc agaaatgata cagcctgtgt gcctgccccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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 0111: 735
 0112: PRT
 0113: Homo sapiens

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 Leu Ala Leu Ala Gly Ala Leu Leu Ala Pro Cys Glu Ala Arg Gly
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 Val Ser Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala
 35 40 45
 Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp
 50 55 60
 Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu
 65 70 75
 Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile
 80 85 90
 Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp
 95 100 105
 Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly
 110 115 120

His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys	135	130	135
Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val	140	145	150
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro	155	160	165
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His	170	175	180
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser	185	190	195
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr	200	205	210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp	275	280	285
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met	395	400	405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly	410	415	420
Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys	425	430	435
Asp Cys Gly Glu Phe Glu Glu Cys Met Asn Arg Cys Cys Asn Ala	440	445	450
Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu	455	460	465
Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg	470	475	480
Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys Phe Ala Asn Val Tyr Leu His Asp Gly His Ser	500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr	515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro	530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro	545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys	560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly	575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr	590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr	605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu	620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln	635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln	650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys	665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly	680	685	690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln
695 700 705

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710 715 720

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725 730 735

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<113> Homo sapiens

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<110> unsure

<120> 3, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<113> unknown base

<100> 75

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ctgacccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400

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<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<100> 76

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<110> 77

<111> 18

<112> DNA

<113> Artificial Sequence

<208>

<209> Synthetic oligonucleotide probe

<401> 77

ctttagcatg tgcacggc 18

<210> 78

<211> 18

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<406> 78

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<409> 79

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<222> 80

<223> 16

<224> DNA

<225> Artificial Sequence

<226>

<227> Synthetic oligonucleotide probe

<400> 80

ctccaggctg gtctccaagt ccttcc 26

<228> 81

<229> 14

<230> DNA

<231> Artificial Sequence

<232>

<233> Synthetic oligonucleotide probe

<409> 81

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<234> 82

<235> 19

<236> DNA

<237> Artificial Sequence

<238>

<239> Synthetic oligonucleotide probe

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<210> 83
<211> 50
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<213> Artificial Sequence

<220>
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<400> 83
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<210> 84
<211> 1714
<212> DNA
<213> Homo sapiens

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<211> 67

<212> PET

<213> Homo sapiens

<400> 35

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				20				25					30	

Thr	Ser	Met	Pro	Glu	Ala	Thr	Ala	Ala	Glu	Thr	Thr	Lys	Pro	Ser
				35				40					45	

Asn	Ser	Ala	Leu	Gln	Pro	Thr	Ala	Gly	Leu	Leu	Val	Val	Leu	Leu
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<211> 23

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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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<213> Homo sapiens

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 <211> 432
 <212> PRT
 <213> Homo sapiens

<400> 90
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 35 40 45

Ala Asp Gly Pro	Pro Ala Ala Asp Gly	Glu Asp Gly Gln Asp	Pro
50	55	60	
His Ser Lys His	Leu Tyr Thr Ala Asp	Met Phe Thr His Gly	110
65	70	75	
Gln Ser Ala Ala	His Phe Val Met Phe	Phe Ala Pro Trp Cys Gly	80
80	85	90	
His Cys Gln Arg	Leu Gln Pro Thr Trp	Asn Asp Leu Gly Asp	100
95	100	105	
Tyr Asn Ser Met	Glu Asp Ala Lys Val	Tyr Val Ala Lys Val Asp	110
110	115	115	
Cys Thr Ala His	Ser Asp Val Cys Ser	Ala Gln Gly Val Arg Gly	125
125	130	135	
Tyr Pro Thr Leu	Lys Leu Phe Lys Pro	Gly Gln Glu Ala Val Lys	140
140	145	145	
Tyr Gln Gly Pro	Arg Asp Phe Gln Thr	Leu Glu Asn Trp Met Leu	155
155	160	165	
Gln Thr Leu Asn	Glu Glu Pro Val Thr	Pro Glu Pro Glu Val Gln	170
170	175	175	
Pro Pro Ser Ala	Pro Glu Leu Lys Gln	Gly Leu Tyr Glu Leu Ser	185
185	190	195	
Ala Ser Asn Phe	Glu Leu His Val Ala	Gln Gly Asp His Phe Ile	200
200	205	210	
Lys Phe Phe Ala	Pro Trp Cys Gly His	Cys Lys Ala Leu Ala Pro	215
215	220	225	
Thr Trp Glu Gln	Leu Ala Leu Gly Leu	Glu His Ser Glu Thr Val	230
230	235	240	
Lys Ile Gly Lys	Val Asp Cys Thr Gln	His Tyr Glu Leu Cys Ser	245
245	250	255	
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260	265	270	
Gly Lys Lys Val	Asp Gln Tyr Lys Gly	Lys Arg Asp Leu Glu Ser	275
275	280	285	
Leu Arg Glu Tyr	Val Glu Ser Gln Leu	Gln Arg Thr Glu Thr Gly	290
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Ala Thr Glu Thr	Val Thr Pro Ser Glu	Ala Pro Val Leu Ala Ala	305
305	310	315	
Glu Pro Glu Ala	Asp Lys Gly Thr Val	Leu Ala Leu Thr Glu Asn	320
320	325	330	

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Glu Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala Gly Val Lys
365 370 375

Ile Ala Glu Val Asp Cys Thr Ala Glu Arg Asn Ile Cys Ser Lys
380 385 390

Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly Gly
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His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu
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<112> DNA

<113> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 93

aaagtggtcgc cttgtgcaac gtgc 24

<210> 94

<211> 13

<212> DNA
<213> Artificial Sequence

<220>
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<400> 94
gggcacagggg gatataatcgc cac 23

<210> 95
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<212> DNA
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<223> Synthetic oligonucleotide probe

<400> 95
gcattgcaaga tgcacaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96
<211> 1016
<212> DNA
<213> Homo sapiens

<400> 96
ctttttctgag gaaccacagc aatgaatggc ttgcatcct tgcttcgaag 50
aaacaaattt atcctcctgg tactatttct ttgcaaaatt cagagtcctgg 100
gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150
atttcaccag gacccaaaagg agatgatggg gaaaaaggag atccaggaga 200
agatggaaag catggcaaa ggggacgcac gggggccgaaa ggaattaaag 250
gagaactggg tgatatggga gatcagggca atattggcaa gactgggccc 300
attgggaaga aggggtgaca aggggaaaaa ggtttgcttg gaatacctgg 350
agaaaaaggc aaagcaggta ctgtctgtga ttgtggaaga taccggaat 400
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ctcctcgtc actatgttg caagagtggc ttcttcggg tgttcattgg 650
cgtgaatgac cttgaaaggg agggacagta catgtccaca gacaacactc 700
cactgcagaa ctatagcaac tggaatgagg gggaaaccag cgaccctat 750
ggtcatgagg actgtgtgga gatgctgagc tctggcagat ggaatgacac 800

agagtgccat cttaccatgt actttgtctg tgagttcacc aagaagaaaa 350
 agtaacttcc ctcatcctac gtatttgcta ttttctgtg accgtcatta 400
 cagttattgt taccatcct tttttctgt attgtactac attgatctg 450
 agtcaacata gctagaaaat gctaaactga ggtatggagg ctccatcacc 1000
 aaaaaaaaaa aaaaaa 1016

<210> 97
 <211> 277
 <212> PFT
 <213> Homo sapiens

<400> 97
 Met Asn Gly Phe Ala Ser Leu Leu Arg Arg Asn Gln Phe Ile Leu
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 Leu Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile
 20 25 30
 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
 35 40 45
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
 50 55 60
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
 65 70 75
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys
 80 85 90
 Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu
 95 100 105
 Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp
 110 115 120
 Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile
 125 130 135
 Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala
 140 145 150
 Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu
 155 160 165
 Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly
 170 175 180
 Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile
 185 190 195
 Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

	200	205	210
Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn			
	215	220	225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser			
	230	235	240
Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly			
	245	250	255
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys			
	260	265	270
Glu Phe Ile Lys Lys Lys Lys			
	275		

<200> 93
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<210>
 <211> Synthetic oligonucleotide probe

<400> 93
 cccggaactat gttgccaaga gtgg 24

<210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<210>
 <211> Synthetic oligonucleotide probe

<400> 99
 gattgatggag gctccatacc tcag 24

<210> 100
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<210>
 <211> Synthetic oligonucleotide probe

<400> 100
 gttgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101
 <211> 3574
 <212> DNA
 <213> Homo sapiens

<400> 101
 gttctatag attcgaattc ggccacactg gccggatcct ctagagatcc 50

ctcgacctcg acccacgcgt cccgtgctct ccccccgtgt ggagtgggtg 100
gggcctgggt gggaatgggc gtgtgcagc gacgcgcgc tccctggaag 150
gagaagtctc agctagaacg agcggccta ggttttcgga agggaggatc 200
agggatgltt gcgagcggt ggaaccagac ggtgcgcata gaggaagcgg 250
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ctttctatt caggctgcg gccgctttag ctactcaag cgggagcgc 550
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ggcagcgcg ggagccgag atgcagcgc cgaagcgcg cggagtttg 700
ccgagggga cggtgccgc agagtgag gagccgcgc cctctgtca 750
cctggagcaa ctgtggcgt gctctccc gctggccag agttctgtg 800
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cgcgcgctg tctggcgcc agattttct ggtccctgg agccgacct 950
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cccacctgc tgaattagc gatctgtg ctgaagtgc cgtgaagtg 1050
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gggtgcacc aggaagatgt gatctactc ggcctccac tctaccat 1250
gtccggttc ctgtgggca tctgggctg catgggcatt ggggcacag 1300
tggtgtgaa atccaagtc tggctgtg agttctgga agattgacg 1350
cagcacagg tgacggtgt ccagtacatt gggagctgt gccgatact 1400
tgtcaaccg ccccgagca aggcagaac tggccataag gtccgctgg 1450

cagtgggcag cggggtgcgc ccagatacct gggagcggtt tgtggggcgc 1500
 ttccggccccc tgcaggtgct ggagacatat ggaactgacag agggcaacgt 1550
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 ccttcgggc ctggggatgt tttcttcaac actggggacc tctgggtctg 1850
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 tatgccggc cccgattctc caggtccag gactctttgg ccaccacaga 2150
 gaccttcaaa cagcagaaag ttccgatggc aaatgagggc ttgcacccca 2200
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 actctajagt cgacctgcag tagggataac agggtaataa gcttggccgc 2550
 catggcccaa cttgtttatt gcag 2574

<210> 100
 <211> 730
 <212> FRT
 <213> Homo sapiens

<400> 100
 Met Gly Val Cys Gln Arg Thr Arg Ala Pro Trp Lys Glu Lys Ser
 1 5 10 15
 Gln Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly
 20 25 30

Met Phe Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala	35	40	45
Gly Ser Met Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu	50	55	60
Pro Leu Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp	65	70	75
Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys	80	85	90
Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Asp Pro	95	100	105
Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu	110	115	120
Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser	125	130	135
Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala	140	145	150
Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp	155	160	165
Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala	170	175	180
Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe	185	190	195
Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro	200	205	210
Leu Ser Pro Gly Ala Thr Val Ala Leu Leu Leu Pro Ala Gly Pro	215	220	225
Glu Phe Leu Trp Leu Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg	230	235	240
Thr Ala Phe Val Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His	245	250	255
Cys Leu Arg Ser Cys Gly Ala Arg Ala Leu Val Leu Ala Pro Glu	260	265	270
Phe Leu Glu Ser Leu Glu Pro Asp Leu Pro Ala Leu Arg Ala Met	275	280	285
Gly Leu His Leu Trp Ala Ala Gly Pro Gly Thr His Pro Ala Gly	290	295	300
Ile Ser Asp Leu Leu Ala Glu Val Ser Ala Glu Val Asp Gly Pro	305	310	315

Val Pro Gly Tyr Leu Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys	320	335	330
Leu Tyr Ile Phe Thr Ser Gly Thr Thr Gly Leu Pro Lys Ala Ala	335	340	345
Arg Ile Ser His Leu Lys Ile Leu Gln Cys Gln Gly Phe Tyr Gln	350	355	360
Leu Cys Gly Val His Gln Glu Asp Val Ile Tyr Leu Ala Leu Pro	365	370	375
Leu Tyr His Met Ser Gly Ser Leu Leu Gly Ile Val Gly Cys Met	380	385	390
Gly Ile Gly Ala Thr Val Val Leu Lys Ser Lys Phe Ser Ala Gly	395	400	405
Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val Thr Val Phe Gln	410	415	420
Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln Pro Pro Ser	425	430	435
Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly Ser Gly	440	445	450
Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly Pro	455	460	465
Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala	470	475	480
Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser	485	490	495
Trp Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp	500	505	510
Val Thr Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met	515	520	525
Ala Thr Ser Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser	530	535	540
Gln Gln Ser Pro Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala	545	550	555
Gln Gly Lys Leu Leu Lys Asp Val Phe Arg Pro Gly Asp Val Phe	560	565	570
Phe Asn Thr Gly Asp Leu Leu Val Cys Asp Asp Gln Gly Phe Leu	575	580	585
Arg Phe His Asp Arg Thr Gly Asp Thr Phe Arg Trp Lys Gly Glu	590	595	600

Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp		
	605	610 615
Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His		
	620	625 630
Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His		
	635	640 645
Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu		
	650	655 660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu		
	665	670 675
Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn		
	680	685 690
Gln Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu		
	695	700 705
Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr		
	710	715 720
Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile		
	725	730

110 103

111 22

112 DNA

113 Artificial Sequence

120

123 Synthetic oligonucleotide probe

400 103

gagagccatg gggctccacc tg 22

110 104

111 18

112 DNA

113 Artificial Sequence

120

123 Synthetic oligonucleotide probe

400 104

gagagaatgtg gccacaac 18

110 105

111 26

112 DNA

113 Artificial Sequence

120

123 Synthetic oligonucleotide probe

<400> 105
gceetggcac agtgactcca tagacg 26

<210> 106
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 106
attacattcca gcggacac 18

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 107
ccatctgcag gatacctctc ttccccccag agcataacag acacg 45

<210> 108
<211> 2579
<212> DNA
<213> Homo sapiens

<400> 108
ccctatgttaa gctgaggttt cccctagatc tcgtatatcc ccaacacata 50
ctctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100
acgggcgcac acacaactgc tctcgtttgt ccatctccct cccggggggag 150
ccgctcgcgcg ctcccacatt tgcgcacac tcgggcgagc cgagcccgc 200
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gggagtggca gtgggtgcat ggatgacgtg tgccccacgg agtttgagtt 2100
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 gatgaaactg catttttagct atctgaatgg ccaactcact tcttttctta 2300
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 ggggtgccaga ctgaactgct tctcttttcc ttcagctatc tgtggggacc 2450
 ttgtttattc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500
 ttcttacctt catttgcttt tatgtgcag aagtaaagga atctcacgtt 2550
 gtgaggggtt ttttttctc atttaaaat 2579

<210> 109

<211> 555

<212> PRT

<213> Homo sapiens

<400> 109

Met	Pro	Ser	Trp	Ile	Gly	Ala	Val	Ile	Leu	Pro	Leu	Leu	Gly	Leu
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Leu	Leu	Ser	Leu	Pro	Ala	Gly	Ala	Asp	Val	Lys	Ala	Arg	Ser	Cys
				20					25					30
Gly	Glu	Val	Arg	Gln	Ala	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ala
				35					40					45
Asp	Ile	Pro	Tyr	Gln	Glu	Ile	Ala	Gly	Glu	His	Leu	Arg	Ile	Cys
				50					55					60
Pro	Gln	Glu	Tyr	Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	Lys	Leu
				65					70					75
Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr
				80					85					90
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe
				95					100					105
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu
				110					115					120
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn
				125					130					135
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr
				140					145					150

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr	170	175	180
His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp	185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln	200	205	210
Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu	215	220	225
Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro	230	235	240
Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro	245	250	255
Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys	260	265	270
Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp	275	280	285
Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu	290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser	320	325	330
Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys	335	340	345
Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe	350	355	360
Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr	365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu	380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr	395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu	410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile	425	430	435

Met	Asn	Asp	Gly	Leu	Thr	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Asp
				440					445					450
Val	Asp	Ile	Thr	Arg	Pro	Asp	Thr	Phe	Ile	Arg	Gln	Gln	Ile	Met
				455					460					465
Ala	Leu	Arg	Val	Met	Thr	Asn	Lys	Leu	Lys	Asn	Ala	Tyr	Asn	Gly
				470					475					480
Asn	Asp	Val	Asn	Phe	Gln	Asp	Thr	Ser	Asp	Glu	Ser	Ser	Gly	Ser
				485					490					495
Gly	Ser	Gly	Ser	Gly	Cys	Met	Asp	Asp	Val	Cys	Pro	Thr	Glu	Phe
				500					505					510
Glu	Phe	Val	Thr	Thr	Glu	Ala	Pro	Ala	Val	Asp	Pro	Asp	Arg	Arg
				515					520					525
Glu	Val	Asp	Ser	Ser	Ala	Ala	Gln	Arg	Gly	His	Ser	Leu	Leu	Ser
				530					535					540
Trp	Ser	Leu	Thr	Cys	Ile	Val	Leu	Ala	Leu	Gln	Arg	Leu	Cys	Arg
				545					550					555

<210> 110

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

aaaggtgaca gcgggcacgt c 21

<210> 111

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 111

tgacagttct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgccctg 40

<21> 113
<211> 4649
<212> DNA
<11> Homo sapiens

<400> 113
ccttcggtg ggagacgag tgggcaanag aactcggagt gccaaageta 50
aataagttag ctgagaaaaac gcacgcagtt tgcagcgect gcgcggggtg 100
cgcaactac gcaagacca agcgggctcc gcgcggaccg gcgcgggggc 150
taaggacccg gctttggcct tcaggctccc tagcagcggg gaaaagggaat 200
tgctgcggg agttctctcg gagggtggagg gagatcagga aacggcttct 250
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 <211> 515
 <212> PRT
 <213> Homo sapiens

<400> 114
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 35 40 45
 Trp Gly Gln Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu Leu Ala
 50 55 60
 Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln
 65 70 75
 Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp
 80 85 90
 Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys
 95 100 105
 Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro
 110 115 120
 Ile Cys Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln
 125 130 135
 Ile His Thr Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro
 140 145 150

Asn Cys Leu Pro	Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys
155	160	165
Glu Val Gly Tyr	Ser Thr His Met Val	Gly Lys Trp His Leu Gly
170	175	180
Phe Asn Arg Lys	Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr
185	190	195
Phe Phe Gly Ser	Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr
200	205	210
Lys Cys Asp Ser	Ile Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn
215	220	225
Asp Asn Ala Ala	Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln
230	235	240
Met Tyr Thr Gln	Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro
245	250	255
Thr Lys Pro Ile	Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser
260	265	270
Pro Leu Gln Ala	Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile
275	280	285
Ile Asn Ile Asn	Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu
290	295	300
Asp Glu Ala Ile	Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly
305	310	315
Phe Tyr Asn Asn	Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly
320	325	330
Gln Pro Thr Ala	Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys
335	340	345
Gly Thr Tyr Trp	Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His
350	355	360
Ser Pro Leu Leu	Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val
365	370	375
His Ile Thr Asp	Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly
380	385	390
Gln Ile Asp Glu	Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu
395	400	405
Thr Ile Ser Glu	Gly Leu Arg Ser Pro	Arg Val Asp Ile Leu His
410	415	420
Asn Ile Asp Pro	Tyr Thr Pro Arg Gln	Lys Met Ala Pro Gly Gln
425	430	435

Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu
					440				445					450
Tys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr
				455					460					465
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly
			470						475					480
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe
			485						490					495
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr
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Gly	Ile	Gln	Glu	Ser										
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 <12> DNA
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<20>
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<210> 116
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 116
 ctctcttgagt gtacatctgt gtgg 24

<210> 117
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<220>
 <221> unsure
 <222> 33
 <223> unknown base

<400> 117
 gccacccctac ctcagaaact gaaggaggtt ggntattcaa cgcatatggt 50

cgg 53

<210> 118

<211> 2260

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086

<223> unknown base

<400> 118

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catgataaac tgtcagtaca gctgtgaaga cacagaagaa gggccacagt 600
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<210> 119

<211> 338

<212> PFT

<213> Homo sapiens

<400> 119

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Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly	
				20					25					30	
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	
				35					40					45	
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	
				50					55					60	
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
				65					70					75	
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	
				80					85					90	
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
				95					100					105	
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	
				110					115					120	
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	
				125					130					135	
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	
				140					145					150	
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	
				155					160					165	
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	
				170					175					180	
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
				185					190					195	
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	
				200					205					210	
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	
				215					220					225	
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	
				230					235					240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	
				245					250					255	
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	
				260					265					270	
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	
				275					280					285	
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
				290					295					300	

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro
305 310 315

Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys
335

<210> 1..9

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 1..9

ctcaggtggc cacatgctca tg 22

<210> 1..11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 1..1

ggctgcacgt atggetatcc atag 24

<210> 1..12

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 1..12

gataaagtgt cagtaacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 1..13

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 1..13

ggagagctgct gctgtggtgt ctgtgtctgt ggcgcctgct cctgctcttg 50

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gggcgaattgg cagggacgac gcccagaatg ggagctgact gatatggttg 150

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<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

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				20					25				30	

Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
				35					40				45	

Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
				50					55				60	

Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val	65	70	75
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly	80	85	90
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr	95	100	105
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr	110	115	120
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile	125	130	135
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser	140	145	150
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn	155	160	165
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser	170	175	180
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser	185	190	195
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln	200	205	210
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile	215	220	225
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro	230	235	240
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala	245	250	255
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe	260	265	270
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys	275	280	285

Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctatggatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

ctcttcagc cactggagg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgttagacat ccaagctggc atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

agaggtctgc atccacacca etc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgcc agaag 46

<210> 131
<211> 2365
<212> DNA
<213> Homo sapiens

<10> 131
ggagcgtggg caacggccatc agctgttccg gcytctttct ctccaggtgg 50
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caatcaatcc aacagcatat tgggttgcac cttctacaca ctacagctat 150
tggttaggtt cctggggaaa cgtggggcct ctgtcttgat gctgctgagc 200
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 tgttacaaaa taaaa 2365

<210> 132
 <211> 571
 <212> PRT
 <213> Homo sapiens

<400> 132
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 20 25 30

Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe	35	40	45
Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn	50	55	60
Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln	65	70	75
Gly Ala His Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val	80	85	90
Leu Thr Ala Ala His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu	95	100	105
Asn Ser Trp Ser Val Val Leu Gly Ser Leu Gln Arg Glu Gly Leu	110	115	120
Ser Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro	125	130	135
Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu	140	145	150
Gln Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln	155	160	165
Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly	170	175	180
Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu	185	190	195
Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn	200	205	210
Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met	215	220	225
Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly	230	235	240
Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp	245	250	255
Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu	260	265	270
Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp	275	280	285
Leu Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro	290	295	300
Glu Thr Pro Glu Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly	305	310	315

Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp
				320					325					330
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly
				335					340					345
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys
				350					355					360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly
				365					370					375
Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	Gln	Leu	Ile	Leu	His	Gly
				380					385					390
Ala	Tyr	Thr	His	Pro	Glu	Gly	Gly	Tyr	Asp	Met	Ala	Leu	Leu	Leu
				395					400					405
Leu	Ala	Gln	Pro	Val	Thr	Leu	Gly	Ala	Ser	Leu	Arg	Pro	Leu	Cys
				410					415					420
Leu	Pro	Tyr	Pro	Asp	His	His	Leu	Pro	Asp	Gly	Glu	Arg	Gly	Trp
				425					430					435
Val	Leu	Gly	Arg	Ala	Arg	Pro	Gly	Ala	Gly	Ile	Ser	Ser	Leu	Gln
				440					445					450
Thr	Val	Pro	Val	Thr	Leu	Leu	Gly	Pro	Arg	Ala	Cys	Ser	Arg	Leu
				455					460					465
His	Ala	Ala	Pro	Gly	Gly	Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met
				470					475					480
Val	Cys	Thr	Ser	Ala	Val	Gly	Glu	Leu	Pro	Ser	Cys	Glu	Gly	Leu
				485					490					495
Ser	Gly	Ala	Pro	Leu	Val	His	Glu	Val	Arg	Gly	Thr	Trp	Phe	Leu
				500					505					510
Ala	Gly	Leu	His	Ser	Phe	Gly	Asp	Ala	Cys	Gln	Gly	Pro	Ala	Arg
				515					520					525
Pro	Ala	Val	Phe	Thr	Ala	Leu	Pro	Ala	Tyr	Glu	Asp	Trp	Val	Ser
				530					535					540
Ser	Leu	Asp	Trp	Gln	Val	Tyr	Phe	Ala	Glu	Glu	Pro	Glu	Pro	Glu
				545					550					555
Ala	Glu	Pro	Gly	Ser	Cys	Leu	Ala	Asn	Ile	Ser	Gln	Pro	Thr	Ser
				560					565					570

Cys

<C10> 133

<C11> 24

<C12> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 133

actgtgtgtgt gcttcgagcc tgac 24

<110> 134

<111> 24

<112> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 134

atgggcagca gtttagcaccg cctc 24

<110> 135

<111> 45

<112> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 135

ggttggtatc atcagctttg catcaagctg tgcccaggag gacgc 45

<110> 136

<111> 1398

<112> DNA

<113> Homo sapiens

<400> 136

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gagccagggt gggccgcgtc cctgagtcgc agagtcggcg ccgcgcggca 100

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gatgtgtgtt cggcggggca gccctggcat ggggtgtcat gtgggtgcag 200

ccctggggagc actgttggtc tgctccacag gaggccctgga ggtccaggtc 250

cctgaagacc cagtgggtgc actgggtggc aacgatgcca cctgtgtctg 300

ctcctttctc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350

ggcagctgac agataccaaa cagctggtgc acagctttgc tgaggggcag 400

gaccagggca ggccttatgc caaccgcacg gccctcttcc cggacctgct 450

ggcacagggc aacgcattcc tgagggtgca ggcggtgggt gtgggggacg 500

agggcagctt cactgtcttc gtgagcatcc gggatttcgg cagcgctgcc 550

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acccaaacaag gacctggcgc caggggacac ggtgaccatc acgtgctcca 650
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attttggggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

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			20					25						30

Val	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp
			35					40						45

Ala	Thr	Leu	Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu
			50					55						60

Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu
			65					70						75

Val	His	Ser	Phe	Ala	Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala
			80					85						90

Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala
			95					100						105

Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe
			110					115						120

Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser
			125					130						135

Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu
			140					145						150

Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys
			155					160						165

Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp
			170					175						180

Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met
			185					190						195

Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val
			200					205						210

Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro
			215					220						225

Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln	
				230					235					240	
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu	
				245					250					255	
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys	
				260					265					270	
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala	
				275					280					285	
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln	
				290					295					300	
Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile	
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Ala

<210> 138
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 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 138
 cgcacacagc tcaaccttat ctgg 24

<210> 139
 <211> 70
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 139
 cgcctgtctgtc tgtctcattg 20

<210> 140
 <211> 20
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 140
 cggacatagta tactgaccac 20

<210> 141
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<410> 141
TGTAAACCAG GCAGTGTAA GTGC 24

<212> 142
<213> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<410> 142
TGTAGAGGA GGGTGGTGT GTGG 24

<212> 143
<213> 45
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<410> 143
TGGTGAAG ACACAAAACA GGTGGTGCA AGTTTCACCG AAGGC 45

<212> 144
<213> 2336
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1620, 1673
<223> unknown base

<400> 144
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GAAGGGGGAG TCTGAACCT GTCTGAAGC CTTGTCCGTA AGCTTGAAC 100
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ACTTCTTTCC TTGCTTCAGC AACATGAGGC TTTCTTGTG GAACGGGTC 200
TTGACTGTGT TGTCACTTC TTTGATTGGG GCTTTGATCC CTGAACCAGA 250
AGTGAAAATT GAAGTTCTCC AGAAGCCATT CATCTGCAT CGCAAGACCA 300
AAGGAGGGGA TTGATGTTG GTCCACTATG AAGGCTACTT AGAAAAGGAC 350
GGCTCCTTAT TTCCTCCAC TCACAAACAT AACAAATGGT AGCCATTGT 400

gtttaccctg ggcacccctg aggtctctca aggttgggac cagggcttga 450
aaggaatgtg tgtaggagag aagagaaaag tcacattcc tctgctctg 500
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atttaatat gatctcttg agattcgaaa tggacaaaga tccctgaat 600
cattccaaga aatggatctt aatgatgaat ggaaaactct taaagatgag 650
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aagacaaaga tgggtttata tctgcagag aatttacata taaaacagat 800
gagtiataga gatacatcta cctttttaat atagacata tttttcaga 850
gagggcagtc atctttaaag aacattttat ttttataaa tgttctctct 900
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 gcagctacta ttgaataaat acctatctgt gatttt 2336

<210> 145
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 145
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 20 25 30
 Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly
 35 40 45
 Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly
 50 55 60
 Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile
 65 70 75
 Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln
 80 85 90
 Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile
 95 100 105
 Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro
 110 115 120
 Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg
 125 130 135
 Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn
 140 145 150

Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys
				155					160					165

Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His
				170					175					180

Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys
				185					190					195

Asp	Gly	Phe	Ile	Ser	Ala	Arg	Glu	Phe	Thr	Tyr	Lys	His	Asp	Glu
				200					205					210

Leu

<210> 146

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 146

tttccattgc ttcagcaaca tgaggc 26

<210> 147

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 147

ggccacagagca ggaggaatga tgagc 25

<210> 148

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 148

gtggaaagcg gtottgaactc tgttcgacac ttctttgatt ggggctttg 49

<210> 149

<211> 2196

<212> DNA

<213> Homo sapiens

<400> 149

aataaagcct ccttaatggt gtatatgtct ttgaagtaca tccgtgcatt 50

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cagagatgac tggctacctc ggcctgcctt cagcctcagc gggctcagtc 200
cttttttctc ttctgtgcca ccaggacgga gcctggaggt cacagtacct 250
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 tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150
 <211> 215
 <212> PET
 <213> Homo sapiens

<400> 150
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 Gly Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met
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 Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp
 35 40 45
 Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His
 50 55 60
 Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys
 65 70 75
 Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu
 80 85 90
 Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro
 95 100 105
 Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu

110	115	120
Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg		
125	130	135
His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu		
140	145	150
Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser		
155	160	165
Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val		
170	175	180
Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp		
185	190	195
Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro		
200	205	210
Asp Asp Gly Ala Lys		
215		

<210> 151

<211> 514

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 103, 233

<223> unknown base

<340> 151

gttgatatg tctgaagta catcgtgca ttttttttag catccaacca 50

tcttcccttg tagttctcgc ccctccaaat cacttctcc cttagccac 100

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gcctgcctt cagcctcagc gggtcagtc tttttttctc tttggtgcca 200

ccaggacgga gcatggaggt ccacagtaac tgnccacct caacgtctc 250

aatggctctg acgcgcgcct gcctgcctt tcaactctg ctacacagt 300

aacacaaaac agttctccct gaactggact taacaggagt gcaacaactg 350

ctctgaggag atgttctcc agttccgcct gaagatcatt aacctgaagc 400

tggagcggtt tcaagaccgc gtggagttct cagggaaccc cagcaagtac 450

gatctgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500

caactgctac atcatgaacc cccc 524

<210> 152

<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 56, 123
<223> unknown base

<400> 152
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ccctgaactg gatttaccag gagtgcacac actggetctg aggagatgtt 200
cttcacgttc ccgcattgaa gatcatttaa cctgaaaagt ggaagcggtt 250
tctcagaacc gcttggaagt ttctcaggga aacccacaa gtaagatctg 300
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ctacatcatg aaccccc 368

<100> 153
<110> 24
<120> DNA
<130> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acgagcatg gaggtccaca gtac 24

<100> 154
<110> 23
<120> DNA
<130> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
ggaagtttct cagcaccacc gac 23

<100> 155
<110> 50
<120> DNA
<130> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155

cgctgacct gaaccttcaa ctctgtctac acagtgaacc acaaacagtt 50

<219> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

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ggctgctcc cggatggact cctgttctc ttgtgtgtgc taatgtgtgt 100
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ctgttgattt gggtaaccaa ctggaagcca agctggacaa gccgacagtg 200
gtgtactacc tctgtccaa gaagaccgaa agctacttca caatctggct 250
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atgctgtataa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

Met	Gly	Leu	His	Leu	Arg	Pro	Tyr	Arg	Val	Gly	Leu	Leu	Pro	Asp
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Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro
			20					25					30

Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
			35						40					45

Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
			50						55					60

Val	His	Tyr	Leu	Gly	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
			65						70					75

Trp	Leu	Asn	Leu	Gln	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
			80						85					90

Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
			95						100					105

Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys
			110						115					120

Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
			125						130					135

Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
			140						145					150

Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
			155						160					165

Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
			170						175					180

Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val
			185						190					195

Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
			200						205					210

Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
			215						220					225

Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
			230						235					240

Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu Leu	
260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu	Lys Val Phe Val Gln Thr	
275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe Gln	
290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu Met	Arg Gln Asp Thr Glu	
305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro	Gly Val Gln Leu His Cys	
320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr Glu	
335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly Asp	
350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp Gln	
365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu	Gln Glu Leu Pro Gly Ser	
380	385	390
Gln His Ile Glu Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr Leu	
395	400	405
Lys Arg Val Leu Leu Gly Pro		
410		

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtagggctg cagaaagtag agcg 24

<210> 150
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 150
gccccaaatg aaaaaggggcc ctacttccctg gccctccgcg agatg 45

<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
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ggcgcgcttc ctgaacgagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150
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<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

Met	Gln	Ser	Gly	Ala	Tyr	Gly	Ala	Ala	Lys	Ala	Gly	Gly	Ser	Phe	1	5	10	15
Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala	20	25	30	
Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly	35	40	45	
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	50	55	60	
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	65	70	75	
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	80	85	90	
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	95	100	105	
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	110	115	120	
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro	125	130	135	
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr	140	145	150	

Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu
				155					160					165

Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn
				170					175					180

Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr
				185					190					195

Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln
				200					205					210

Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr
				215					220				

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<230> 163

<231> ctgcttcggc cttgategtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<230> 164

<231> gtgtactgag cggcgggtag 20

<210> 165

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<230> 165

<231> ctgaaggtga tggctgccct cac 23

<210> 166

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 166
ccaggaggct catgggaaag tcc 23

<210> 167

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 167

ccacgagtct aagcagatgt actgogtggt caaccgcaac gaggatgct 50

<210> 168

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 168

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ctggcgggca ggggagcga ggtgatggcg aggaagcgga gccagagggg 150
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 Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val
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Leu Glu Ala Ser Val Lys Asp Ile Ala Ala Leu Asn Ser Thr Leu		
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Gln Gly Pro Lys Asp Leu Met Leu Lys Leu Arg Leu Glu Trp Thr		
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Leu Ala Glu Cys Arg Asp Arg Leu Ala Met Tyr Asp Val Ala Gly		
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Pro Leu Glu Lys Arg Leu Ile Thr Ser Val Tyr Gly Cys Ser Arg		
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Asp Gly Val Lys	Asp Cys Pro Asn Gly	Leu Asp Glu Arg Asn	Cys		
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Ala Ser Thr Val	Leu Trp Thr Val Phe	Leu Gly Lys Val Trp	Gln		
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Asn Ser Arg Trp	Pro Gly Glu Val Ser	Phe Lys Val Ser Arg	Leu		
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Leu Leu His Pro	Tyr His Glu Glu Asp	Ser His Asp Tyr Asp	Val		
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Ala Leu Leu Gln	Leu Asp His Pro Val	Val Arg Ser Ala Ala	Val		

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<223> Synthetic oligonucleotide probe

<400> 172

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<212> DNA

<213> Homo sapiens

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His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu	65	70	75	
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<212> DNA

<213> Homo sapiens

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gatgcagcc ctggtacgcc gtctccggcg ctggggcttg ctccctcgaa 2250
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gtgtctcccc tgaggccct agatggtggc acaggtccag cccgtgaggg . 350
cggggcagtg ggtgggcaag atggggagca ggcaccccca ctgcccacca 2400
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gaagcccccag ggccactgcc ctcaactgccc ctagagccat cactattgtc 2500
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gccatggcca gacaccccag tcccttcacc accacctgct ccccacgcca 2950
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 caccggaatg ccaattaaat agagacctc cagcccccaa ggggaggatt 3100
 tgggcagaac ctgagggttt gccatccaca atccctctta cagggccttg 3150
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<110> 183

<111> 713

<112> PBT

<113> Homo sapiens

<100> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu	1	5	10	15	
Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp	20	25	30	
Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro	35	40	45	
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu	50	55	60	
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys	65	70	75	
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro	80	85	90	
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu	95	100	105	
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly	110	115	120	
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln	125	130	135	
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His	140	145	150	
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys	155	160	165	
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro	170	175	180	
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr				

145	190	195
Leu Glu Asp Phe Tyr Gly Val Phe Ser	Ser Pro Gly Tyr Thr His	
200	205	210
Leu Ala Ser Val Ser His Pro Gln Ser	Cys His Trp Leu Leu Asp	
215	220	225
Pro His Asp Gly Arg Arg Leu Ala Val	Arg Phe Thr Ala Leu Asp	
230	235	240
Leu Gly Phe Gly Asp Ala Val His Val	Tyr Asp Gly Pro Gly Pro	
245	250	255
Pro Glu Ser Ser Arg Leu Leu Arg Ser	Leu Thr His Phe Ser Asn	
260	265	270
Gly Lys Ala Val Thr Val Glu Thr Leu	Ser Gly Gln Ala Val Val	
275	280	285
Ser Tyr His Thr Val Ala Trp Ser Asn	Gly Arg Gly Phe Asn Ala	
290	295	300
Thr Tyr His Val Arg Gly Tyr Cys Leu	Pro Trp Asp Arg Pro Cys	
305	310	315
Gly Leu Gly Ser Gly Leu Gly Ala Gly	Gln Gly Leu Gly Glu Arg	
320	325	330
Cys Tyr Ser Glu Ala Gln Arg Cys Asp	Gly Ser Trp Asp Cys Ala	
335	340	345
Asp Gly Thr Asp Glu Glu Asp Cys Pro	Gly Cys Pro Pro Gly His	
350	355	360
Phe Pro Cys Gly Ala Ala Gly Thr Ser	Gly Ala Thr Ala Cys Tyr	
365	370	375
Leu Pro Ala Asp Arg Cys Asn Tyr Gln	Thr Phe Cys Ala Asp Gly	
380	385	390
Ala Asp Glu Arg Arg Cys Arg His Cys	Gln Pro Gly Asn Phe Arg	
395	400	405
Cys Arg Asp Glu Lys Cys Val Tyr Glu	Thr Trp Val Cys Asp Gly	
410	415	420
Gln Pro Asp Cys Ala Asp Gly Ser Asp	Glu Trp Asp Cys Ser Tyr	
425	430	435
Val Leu Pro Arg Lys Val Ile Thr Ala	Ala Val Ile Gly Ser Leu	
440	445	450
Val Cys Gly Leu Leu Leu Val Ile Ala	Leu Gly Cys Thr Cys Lys	
455	460	465
Leu Tyr Ala Ile Arg Thr Gln Glu Tyr	Ser Ile Phe Ala Pro Leu	

	470	475	480
Ser Arg Met Glu	Ala Glu Ile Val Gln	Gln Gln Ala Pro Pro Ser	
	485	490	495
Tyr Gly Gln Leu	Ile Ala Gln Gly Ala	Ile Pro Pro Val Glu Asp	
	500	505	510
Phe Pro Thr Glu	Asn Pro Asn Asp Asn	Ser Val Leu Gly Asn Leu	
	515	520	525
Arg Ser Leu Leu	Gln Ile Leu Arg Gln	Asp Met Thr Pro Gly Gly	
	530	535	540
Gly Pro Gly Ala	Arg Arg Arg Gln Arg	Gly Arg Leu Met Arg Arg	
	545	550	555
Leu Val Arg Arg	Leu Arg Arg Trp Gly	Leu Leu Pro Arg Thr Asn	
	560	565	570
Thr Pro Ala Arg	Ala Ser Glu Ala Arg	Ser Gln Val Thr Pro Ser	
	575	580	585
Ala Ala Pro Leu	Gln Ala Leu Asp Gly	Gly Thr Gly Pro Ala Arg	
	590	595	600
Glu Gly Gly Ala	Val Gly Gly Gln Asp	Gly Glu Gln Ala Pro Pro	
	605	610	615
Leu Pro Ile Lys	Ala Pro Leu Pro Ser	Ala Ser Thr Ser Pro Ala	
	620	625	630
Pro Thr Thr Val	Pro Glu Ala Pro Gly	Pro Leu Pro Ser Leu Pro	
	635	640	645
Leu Glu Pro Ser	Leu Leu Ser Gly Val	Val Gln Ala Leu Arg Gly	
	650	655	660
Arg Leu Leu Pro	Ser Leu Gly Pro Pro	Gly Pro Thr Arg Ser Pro	
	665	670	675
Pro Gly Pro His	Thr Ala Val Leu Ala	Leu Glu Asp Glu Asp Asp	
	680	685	690
Val Leu Leu Val	Pro Leu Ala Glu Pro	Gly Val Trp Val Ala Glu	
	695	700	705
Ala Glu Asp Glu	Pro Leu Leu Thr		
	710		

02100 184

02110 20

02120 DNA

02130 Artificial Sequence

02200

02230 Synthetic oligonucleotide probe

<400> 184

ggtgtgact gtggagacac 20

<210> 185

<211> 18

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 185

gagatcat tacagctg 18

<210> 186

<211> 13

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 186

tttcatagg agcagtccca ctc 23

<210> 187

<211> 13

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 187

tttctgtgc tgcacaatct cag 23

<210> 188

<211> 45

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 188

ggctattgct tgcottggga cagacctgt ggcttaggct ctggc 45

<210> 189

<211> 663

<212> DNA

<213> Homo sapiens

<400> 189

cgagctgggc gagaagtagg ggagggcggg gtcgccgc ggtggcggtt 50

ggtatcggtt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgtgt ctgctgggtc tgcagacggc atggataacg tgcagccgaa 150
 aataaaacat cgcctctctt gcttcagtgt gaaagggcac gtgaagatgc 200
 tggggctggc actaacgtgt acatctatga ccttttttat catcgacaaa 250
 gcccctgaac catataatgt tatcactgga ttggaagtea ccgttatott 300
 atttttcata cttttatgtg tactcagact tgcctgatta atgaagtggc 350
 tattttggcc ttgcttgat attatcaact cactggtaac aacagtattc 400
 atgctcatcg tatctgtgtt ggcactgata ccagaaacca caacattgac 450
 agttgggtga ggggtgttg cacttgtagc agcagtatgc tgtcttgccg 500
 acggggccct tatttaacgg aagcttctgt tcaatcccag cggctcctac 550
 cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600
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 aaaaaaaaaa aaa 660

<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<100> 190

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe
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Ser	Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Ala	Leu	Thr	Val
			20						25					30
Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr
			35						40					45
Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile
			50						55					60
Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe
			65						70					75
Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe
			80						85					90
Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr
			95						100					105
Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys
			110						115					120
Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn
			125						130					135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
 140 145 150

Val Leu

<210> 191
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 78, 212, 234, 487
 <223> unknown base

<400> 191
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 ctgtctgtcg gtcctgcagac cgcgtggata acgtgcagcc gaaaataaaa 150
 catcgccctt tctgtttcag tgtgaaaggg caagtgaaaga tgetgnggct 200
 ggcactaaact gngacatcta tgaccttttt tatnctcgca caagcccttg 250
 aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300
 ataacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350
 ggcctttgctt gatattatca actcactggg aacaacagta ttcattgtca 400
 tgcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450
 ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 192
 ggttttcag aacctactca ggcag 25

<210> 193
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 193
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 194
aaagtgtctgc tcttgggtct gcagacgcga tggataacgt 40

<210> 195
<211> 1879
<212> DNA
<213> Homo sapien

<400> 195
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ggacccgcta ggttgggcgc gccccccggg ccccgccgtg ggcattgggcg 100
caactggcccg ggcgtctctg ctgcctctgc tggccagtg gctcctgcgc 150
ggcgcccccg agctggcccc cgcgccttc acgtgcccc tccgggtggc 200
cgcgcccaag aaccgcgtag ttgcgcacc cccgggaccc gggacccctg 250
ccgagcgcca ccgcgaaggc ttggcgctcg cctgggagcc tgcctggcg 300
tcccccgccg gcgcgcacca cttcttggcc atggtagaca acctgcaggg 350
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agaagctaca gattctcgtt gacactggaa gcagtaactt tgccttggca 450
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cacataccgc tccaagggtt ttgacgtcac agtgaagtac acacaaggaa 550
gctgggaaggg cttcgttggg gaagacctcg tcaccatccc caaaggcttc 600
aatactctt tcttctgcaa cattgcact atttttgaat cagagaattt 650
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acacaaggca acatccccc cgtttttctc atgcagatgt gtggagccgg 800
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 ctggaactggg tcccagctgg cgtgctggac gaattcggaa acaccttggt 1150
 cttacttccc taaaatctcc atctacctga gagacgagaa ctccagcagg 1200
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 atgcgctggg gatcgggtgc accgtgatgg agggcttcta cgtcatcttc 1350
 gacagagccc agaagagggg gggcttcgca gcgagcccct gtgcagaaat 1400
 tgcaggtgct gcagtgctg aaatttcgg gcctttctca acagaggatg 1450
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 aaataattaa aaaaaaaact tcattctaa 1879

<E10> 196

<E11> 518

<E12> PFT

<E13> Homo sapien

<I40> 196

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Trp	Leu	Leu	Arg	Ala	Ala	Pro	Glu	Leu	Ala	Pro	Ala	Pro	Phe	Thr
			20						25				30	
Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Thr	Asn	Arg	Val	Val	Ala	Pro
			35						40				45	
Thr	Pro	Gly	Pro	Gly	Thr	Pro	Ala	Glu	Arg	His	Ala	Asp	Gly	Leu
			50						55				60	

Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala	
				65					70					75	
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg	
				80					85					90	
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu	
				95					100					105	
Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly	
				110					115					120	
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser	
				125					130					135	
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr	
				140					145					150	
Ala	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile	
				155					160					165	
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile	
				170					175					180	
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly	
				185					190					195	
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser	
				200					205					210	
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro	
				215					220					225	
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala	
				230					235					240	
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu	
				245					250					255	
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu	
				260					265					270	
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly	
				275					280					285	
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala	
				290					295					300	
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val	
				305					310					315	
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro	
				320					325					330	
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp	
				335					340					345	

Thr Asn Ser Glu	Thr Pro Trp Ser Tyr	Phe Pro Lys Ile Ser	Ile
350		355	360
Tyr Leu Arg Asp	Glu Asn Ser Ser Arg	Ser Phe Arg Ile Thr	Ile
365		370	375
Leu Pro Gln Leu	Tyr Ile Gln Pro Met	Met Gly Ala Gly Leu	Asn
380		385	390
Tyr Glu Cys Tyr	Arg Phe Gly Ile Ser	Pro Ser Thr Asn Ala	Leu
395		400	405
Val Ile Gly Ala	Thr Val Met Glu Gly	Phe Tyr Val Ile Phe	Asp
410		415	420
Arg Ala Gln Lys	Arg Val Gly Phe Ala	Ala Ser Pro Cys Ala	Glu
425		430	435
Ile Ala Gly Ala	Ala Val Ser Glu Ile	Ser Gly Pro Phe Ser	Thr
440		445	450
Glu Asp Val Ala	Ser Asn Cys Val Pro	Ala Gln Ser Leu Ser	Glu
455		460	465
Pro Ile Leu Trp	Ile Val Ser Tyr Ala	Leu Met Ser Val Cys	Gly
470		475	480
Ala Ile Leu Leu	Val Leu Ile Val Leu	Leu Leu Leu Pro Phe	Arg
485		490	495
Cys Gln Arg Arg	Pro Arg Asp Pro Glu	Val Val Asn Asp Glu	Ser
500		505	510
Ser Leu Val Arg	His Arg Trp Lys		
515			

*210> 197

*211> 21

*212> DNA

*213> Artificial Sequence

*220>

*223> Synthetic oligonucleotide probe

*400> 197

ggagaagct acagattctc g 21

*210> 198

*211> 19

*212> DNA

*213> Artificial Sequence

*220>

*223> Synthetic oligonucleotide probe

*400> 198

ggaaattgga ggccaaagc 19

<210> 199
<211> 20
<212> PNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 199
ggatgtaqcc agcaactgtg 20

<210> 200
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 200
agcttaqctc gttctcttc 19

<210> 201
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 201
agctctctgc ctggatgg 18

<210> 202
<211> 21
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 202
agacaagacta cctcagttgg tc 22

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 203
tgatgacag ttcagcaact gttg 24

<210> 204

<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 204
tgcctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205
<211> 1939
<212> DNA
<213> Homo sapiens

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<E10> 206

<E11> 377

<E12> PFT

<E13> Homo sapiens

<F00> 206

Met	Glu	Ala	Leu	Leu	Leu	Gly	Ala	Gly	Leu	Leu	Leu	Gly	Ala	Tyr
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Val	Leu	Val	Tyr	Tyr	Asn	Leu	Val	Lys	Ala	Pro	Pro	Cys	Gly	Gly
				20					25					30

Met	Gly	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Val	Val	Thr	Gly	Ala	Asn
				35					40					45

Ser	Gly	Ile	Gly	Lys	Met	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Arg	Gly
				50					55					60

Ala	Arg	Val	Val	Leu	Ala	Cys	Arg	Ser	Gln	Glu	Arg	Gly	Glu	Ala
				65					70					75

Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile	90	90
Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe	95	105
Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile	110	120
His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe	125	135
Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr	140	150
His Leu Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val	155	165
Val Val Val Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Ile	170	180
Lys Arg Leu Asp Arg Pro Val Val Gly Trp Arg Gln Glu Leu Arg	185	195
Ala Tyr Ala Asp Thr Lys Leu Ala Asn Val Leu Phe Ala Arg Glu	200	210
Leu Ala Asn Gln Leu Glu Ala Thr Gly Val Thr Cys Tyr Ala Ala	215	225
His Pro Gly Pro Val Asn Ser Glu Leu Phe Leu Arg His Val Pro	230	240
Gly Trp Leu Arg Pro Leu Leu Arg Pro Leu Ala Trp Leu Val Leu	245	255
Arg Ala Pro Arg Gly Gly Ala Gln Thr Pro Leu Tyr Cys Ala Leu	260	270
Gln Glu Gly Ile Glu Pro Leu Ser Gly Arg Tyr Phe Ala Asn Cys	275	285
His Val Glu Glu Val Pro Pro Ala Ala Arg Asp Asp Arg Ala Ala	290	300
His Arg Leu Trp Glu Ala Ser Lys Arg Leu Ala Gly Leu Gly Pro	305	315
Gly Glu Asp Ala Glu Pro Asp Glu Asp Pro Gln Ser Glu Asp Ser	320	330
Glu Ala Pro Ser Ser Leu Ser Thr Pro His Pro Glu Glu Pro Thr	335	345
Val Ser Gln Pro Tyr Pro Ser Pro Gln Ser Ser Pro Asp Leu Ser	350	360

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln
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Ile Ser

<210> 107

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 107

cttcattggcc ttggacttgg ccag 24

<210> 209

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 108

acggccactgg cctcaagctg gttg 24

<210> 209

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 209

ctttctcagc tctgagccac ggttggaacat cctcatccac aatgc 45

<210> 110

<211> 3716

<212> DNA

<213> Homo sapiens

<400> 210

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caagcctcag gccagccacc tcccaccatc cgtctgggtgc tgaatgggca 200

gcccttgagc atgggtgcccc cagaccacaa ccacctcttg cctgatggga 250

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 <212> PFT
 <213> Hcno sapiens

<400> 211
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 20 25 30
 Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu
 35 40 45
 Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu
 50 55 60
 Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg Gly
 65 70 75
 His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr
 80 85 90
 Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly
 95 100 105
 Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln
 110 115 120
 Pro Arg Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu
 125 130 135

Cys Gly Pro Pro	Trp Gly His Pro Glu	Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys	Pro Leu Ala Leu Gln	Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser	Leu Leu Met Ala Arg	Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met	Cys Val Ala Thr Asn	Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala	Arg Val Ser Ile Gln	Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu	Leu Leu Ala Val Arg	Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn	Pro Asp Pro Ala Glu	Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu	Ser Trp Lys Val Ser	Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr	Ala Leu Phe Arg Thr	Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro	Trp Ala Glu Glu Leu	Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly	Gly Leu His Trp Gly	Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser	Ser Gly Arg Ala Arg	Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg	Leu Pro Glu Lys Val	Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu	Lys Pro Gly Asn Gly	Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro	Ala Glu Asn His Asn	Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser	Leu Gly Asn Thr Ser	Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly	Glu Gln Thr Gln Leu	Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr	Cys Val Gln Val Ala	Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro	Ser Arg Pro Val Cys	Leu Leu Leu Glu Gln Ala	410	415	420

Met Glu Arg Ala Thr Gln Glu Pro Ser	Glu His Gly Pro Trp Thr
425	435
Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala	
440	450
Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val	
455	465
Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly	
470	480
Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met	
485	495
Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr	
500	510
Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg	
515	525
Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu	
530	540
Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp	
545	555
Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser	
560	570
Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu	
575	585
Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp	
590	600
Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu	
605	615
Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln	
620	630
His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu	
635	645
Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser	
650	660
Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala	
665	675
Leu Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg	
680	690
His Leu Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr	
695	705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser	710	715	720
Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys	725	730	735
Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro	740	745	750
Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu	755	760	765
Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu	770	775	780
Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro	785	790	795
Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser	800	805	810
Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly	815	820	825
Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro	830	835	840
Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp	845	850	855
Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu	860	865	870
Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala	875	880	885
Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu	890	895	900
Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro	905	910	915
Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro	920	925	930
Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser	935	940	945
His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp	950	955	960
Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro	965	970	975
Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser	980	985	

<210> 212
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 212
gaaggaacct acatgttgtt ggcc 24

<210> 213
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<220>
<221> Synthetic oligonucleotide probe

<400> 213
atgaacatc cagctgagcc acaac 24

<210> 214
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<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 214
atpactaac ggagcctgtg gagcttcttg ctgtgcgaat tcagctggaa 50

<210> 215
<211> 2749
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1869, 1887
<223> unknown base

<400> 215
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(210) 216

(211) 332

(212) PRT

(213) Homo sapiens

(400) 216

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly
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Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly
			20						25				30	

Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp
			35					40					45	

His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Cys Ser Gly Thr Ile Tyr Ala Glu Glu Gln Gly Gln Glu Thr Met		
65	70	75
Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu		
80	85	90
Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr		
95	100	105
Trp Cys Gly Val Gln Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile		
110	115	120
Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser		
125	130	135
Pro Thr Phe Gln Phe Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala		
140	145	150
Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu		
155	160	165
Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu		
170	175	180
Ala Pro Pro Leu Phe Gly Thr Ser Gln Tyr Gly His Glu Arg Thr		
185	190	195
Ser Gln Tyr Thr Gly Thr Ser Pro His Phe Ala Thr Ser Pro Phe		
200	205	210
Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala		
215	220	225
Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg		
230	235	240
Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu		
245	250	255
Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His		
260	265	270
Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln		
275	280	285
Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys		
290	295	300
Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro		
305	310	315
Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val		
320	325	330
Ser Ala		

<210> 217

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 217

ccctgcagtg cacctacagg gaag 24

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 218

ctctctcccc ctgcttggt gtgg 24

<210> 219

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 219

gggtccaggaa ggggtgggac ctctctctc gctgctctg ccacatc 47

<210> 220

<211> 950

<212> DNA

<213> Homo sapiens

<400> 220

ttgtgactaa aagctggcct agcagggcag ggagtgcagc tgcaggcgtg 50

ggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100

cagtgtgaaa gaaccagtgg tctcgtcttg ttgccaggc tagagtgtac 150

tggcgtgac atagctcact gcagcctcag actcctggac ttgagaaatc 200

ctctggtctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250

cctgtttctt ctctctctgt gagtggacca cggagggttg tgagctgact 300

gtcatcctaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350

ccgcgcgcct agaagccagg agcagggctc tcagaaggcg gtggtgccca 400

ctctgagatca tgttgtttgga cctggtcttgt ctgctcagct goctgtctacc 450
 ctctgagtgag gccaaacctct acgtgagttg tgaactggcc agagtgtctac 500
 ctctcttggg gctggacgga taatggggat acagcctggc tgaactggtc 550
 ctcttctgtt atttcacaag cgttttcaac gcagctgctt tggactacga 600
 ggttatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650
 ctgtaagaaa cctcaccctcg aacgtcccca acgtgtgccg gatgtactgc 700
 ctgattttgt tgaatcccaa tctcaggat accgttatct gtgccatgaa 750
 ctctacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
 actgcccagg aaaagacctc actgaatggg tggatggctg tgaattctag 850
 ctatgaaggga accatgcaca gaaggetggg aaatgtgggt tggttcctga 900
 ctctgctttg ggaagacaag ctatggcata aaggatgggt gaaagtgaaa 950

<210> 221
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 221
 Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser
 1 5 10 15
 Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu
 20 25 30
 His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp
 35 40 45
 Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala
 50 55 60
 Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln
 65 70 75
 Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro
 80 85 90
 Asn Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu
 95 100 105
 Lys Asp Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln
 110 115 120
 Gly Leu Gly Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys
 125 130 135
 Asp Leu Thr Glu Trp Val Asp Gly Cys Asp Phe
 140 145

<210> 222
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 222
ggatcatgt tgttgccct ggtc 24

<210> 223
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 223
gagagaga cccagtcagc cag 23

<210> 224
<211> 4
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 224
ctgcctgcta cctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225
<211> 1049
<212> DNA
<213> Homo sapiens

<400> 225
agcagctgac cggggcggg cgcgcgggc gccaccatga gtcccgcctc 50
jtgcctgggt tcgtgcgac tctcgtctt cgcgctcttc tcagccgcgc 100
cgagcactg gctgtacct gccaaagtgt cgtcgggtgg gagcatctca 150
gaggaagaga cgtgcgagaa actcaagggc ctgatccaga gccaggtgca 200
gatgtcaag cggaaacctg aagtcattga ctcgggtgcgc cgcggtgcac 250
agctggcat tgaggagtgc cagtaccagt tcgggaacgc gcgctggaac 300
tgcctccac tcgaactctt gccgctcttc ggcaagggtg tgacgcaagg 350
gaactcggag ggggccttcg tgtaagcat ctcttcggca ggtgtggcct 400
ttgcagtgac gggggcgtgc agcagtggg agctggagaa gtgcggctgt 450

gacaggacag tgcattgggt cagcccacag ggcttccagt ggtcaggatg 500
ctctgacaa ctcgcttact gtgtggcctt ctccacagtc ttgttgatg 550
tccatagag aacatagtg cctctctc cagagatct ctggaactc 600
cacaacaatg agctcgtcag gaaggccatc ctgacacaca tgcgggtgga 650
atccagtac caatgggtgt caggtctctg tgaagtaag acgtcctgg 700
cagccttgcg ggccttcgc caggtgggtc acgcactga gagagaagttt 750
gatggtgcca ctgaggtgga gccacgcgc gtgggtcct ccagggcact 800
ggtaccacgc aagccacagt tcaagcgc caacatgag gacctggtgt 850
acttgagagc tagtccgc ttctatgagc aggcactgc cagcggcgtg 900
ctgggacga gggtgcgc atgcaaac agtccaaag ccctcgacgg 950
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cggaagtgc aggggtcgt aggttgca acgtgcgat gaccgcctgc 1100
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aaacagtct cccaccta cccaagaga tactggtgt attttttgtt 1200
ctggtttggt ttttggtcc tcatgtatt tattgcgaa accaggcagg 1250
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gtgccactg accactcagt tgttatctgt gtcgtttt ctacttgag 1400
acctaaagt gagtaaca gagtattacc accacatgc tactgacgt 1450
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gcaagaagag ggagatgaga gcaagagac actgaagtc caccctagaa 1750
cccagcctgc ccagcctgc cctgggaag aggaaacta accactcccc 1800
agaccacct aggcaggcat ataggtgc atcctggacc agggatcccc 1850

gctgtgcctt tgcagtcatt gccagtcac ctttcacagc gctgttcctc 1900
 catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950
 acacacacac ggaracacac acacacctgc gagagacacg gaggaagagg 2000
 cgtgcctttt acagtcattg ccagtcacac tttcacagca ctgttcctc 2049

<210> 226
 <211> 351
 <212> FRT
 <213> Homo sapiens

<400> 226
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 1 5 10 15
 Ala Val Phe Ser Ala Ala Ala Ser Asn Trp Leu Tyr Leu Ala Lys
 20 25 30
 Leu Ser Ser Val Gly Ser Ile Ser Glu Glu Glu Thr Cys Glu Lys
 35 40 45
 Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn
 50 55 60
 Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile
 65 70 75
 Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser
 80 85 90
 Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly
 95 100 105
 Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val
 110 115 120
 Ala Phe Ala Val Thr Arg Ala Cys Ser Ser Gly Glu Leu Glu Lys
 125 130 135
 Cys Gly Cys Asp Arg Thr Val His Gly Val Ser Pro Gln Gly Phe
 140 145 150
 Gln Trp Ser Gly Cys Ser Asp Asn Ile Ala Tyr Gly Val Ala Phe
 155 160 165
 Ser Gln Ser Phe Val Asp Val Arg Glu Arg Ser Lys Gly Ala Ser
 170 175 180
 Ser Ser Arg Ala Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg
 185 190 195
 Lys Ala Ile Leu Thr His Met Arg Val Glu Cys Lys Cys His Gly
 200 205 210
 Val Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Arg Ala Val Pro

215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly		
230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu		
245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu		
260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg		
275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser		
290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe		
305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe		
320	325	330
His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val		
335	340	345
Glu Leu His Thr Cys Arg		
350		

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 228

tggtgggaga ctgtttaaat tatcggcc 28

<210> 229

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgtttctctca agtctccgga gtgctcagg ctcctcaggt t 41

<210> 229

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

cggaagcctg ggcgaacgg tgggcaggc cgtgggaga cgcctgggt 50
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gttcggagga ggtcccgga gggccctgg gacatcaggt gaactggag 150
aggagaccc tctctctggc cctggctgtc ctggtacaa cagtcctttg 200
ggctgtgatt ctgagtatcc tattgtccaa ggcttcacg gaggcgagg 250
cgtctcttga cggcaccag ctcctcagga caaatcttc gaacagagc 300
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cactgagctg ttccgggggc tggaggccgt gaggctccag aacaactcct 550
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tctcattcca ccgtctgtga gtctcagaaa caattggccc aacatagccc 1100
tgtccagccc agtgcctggg ctctgggaac tccatgccga cctcattcta 1150

actccactca cgcagaccga acctaacctc cactagctcc aaaatccctg 1200
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 gtgactgagg actggagctg tttgggtttc tgcgattttc caccaaaactg 1300
 gaagctgttt ttgcagcctg aggaagcacc aataaatatt tgagaaatga 1350
 aaaaa 1355

<210> 231
 <211> 293
 <212> PRT
 <213> Homo sapiens

<400> 231
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 1 5 10 15
 Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg
 20 25 30
 Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp
 35 40 45
 Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg
 50 55 60
 Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser
 65 70 75
 Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp
 80 85 90
 Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr
 95 100 105
 Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu
 110 115 120
 Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala
 125 130 135
 Glu Ala Gly Arg Gly Arg Glu Asp Val Arg Thr Glu Leu Phe Arg
 140 145 150
 Ala Leu Glu Ala Val Arg Leu Gln Asn Asn Ser Cys Glu Pro Cys
 155 160 165
 Pro Thr Ser Trp Leu Ser Phe Glu Gly Ser Cys Tyr Phe Phe Ser
 170 175 180
 Val Pro Lys Thr Thr Trp Ala Ala Ala Gln Asp His Cys Ala Asp
 185 190 195
 Ala Ser Ala His Leu Val Ile Val Gly Gly Leu Asp Glu Gln Gly
 200 205 210

Phe Leu Thr Arg Asn Thr Arg Gly Arg Gly Tyr Trp Leu Gly Leu
215 220 225

Arg Ala Val Arg His Leu Gly Lys Val Gln Gly Tyr Gln Trp Val
230 235 240

Asp Gly Val Ser Leu Ser Phe Ser His Trp Asn Gln Gly Glu Pro
245 250 255

Asn Asp Ala Trp Gly Arg Glu Asn Cys Val Met Met Leu His Thr
260 265 270

Gly Leu Trp Asn Asp Ala Pro Cys Asp Ser Glu Lys Asp Gly Trp
275 280 285

Ile Cys Glu Lys Arg His Asn Cys
290

<110> 132

<111> 14

<112> DNA

<113> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 132

ccgagaactg tgtcatgatg ctgc 24

<110> 133

<111> 14

<112> DNA

<113> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

gtttctgaga ctccgcagcg gtgg 24

<110> 134

<111> 50

<112> DNA

<113> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

ccacgtgtga cagcgagaag gacgggtgga tctgtgagaa aaggcacaac 50

<110> 135

<111> 1547

<112> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gaggtgata cgacccgggg aaggtegetg ggcagggcga 50
gttgggaaag cggcagcccc cgcgcgcgcc gcagcccctt ctctctcttt 100
ctcccacgtc ctatctgcct ctctctggag gccaggccgt gcagatcga 150
agacaggag aactggagcc tcattggccc gcccgggccc cgggcctcgg 200
gcttaaatag gagctccggg ctctggcttg gacccgaccg ctgcggggcg 250
cgctcccgt gctcctgcgc ggtgatgga aaccccagcc cggccgcgcg 300
cctgggcaag gccctctgcg ctctctctct ggccactctc ggccgcgcgc 350
gccagcctct tgggggagag tccatctgtt ccgcagagc cccgcacaaa 400
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gtaccccctg ttcgccccc ctgcgcagtg gcttctcctg ctggggggcg 500
cgcatacctc cgaactacgc atgtggagga aqaaccagta cgtcagtaac 550
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gacgcaggcg ggggggaggg cgtgcagag cgtgcacgag gtgttttcgg 650
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ggtgaccgag ataangtct cctctcccag ccaaccggcc aactccttct 950
actaccgcg gctgaaggcc ctgcctccca tcgcacagggt gacactgctg 1000
cggctgcgac agagcccccag ggcttccatc cctcccgcgc cagtctgcgc 1050
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tggaactcga ggtctccctg ttgtcgtcct ggggaactgt cggaggccac 1150
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cgccaacac cggagccccc gccccgagct cgaagaagag gctgagtgcg 1250
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cggagccatg ggtgtcggg ggtcctgtg caggctcatg ctgcaggcgg 1350
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cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450
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 tgtcttctat cgtccagggg cctgggtccc acgtggttgc agatacctca 1650
 gaactgggtgc tctaggtgt gctgagccca ctctccgag ggcgcaccca 1700
 agcggggggc acttgagaag tgaataaatg gggcggttgc ggaagcgtca 1750
 gtgtttccat gttatgcac tctctgcgtt tgaataaaga ctatctctgt 1800
 tgcacacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 131

<212> F5T

<213> Homo sapiens

<400> 236

Met	Glu	Asn	Pro	Ser	Pro	Ala	Ala	Ala	Leu	Gly	Lys	Ala	Leu	Cys
1				5					10					15
Ala	Leu	Leu	Leu	Ala	Thr	Leu	Gly	Ala	Ala	Gly	Gln	Pro	Leu	Gly
				20					25					30
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile
				35					40					45
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr
				50					55					60
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala
				65					70					75
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val
				80					85					90
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala
				95					100					105
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val
				110					115					120
His	Glu	Val	Phe	Ser	Ala	Pro	Ala	Val	Pro	Ser	Gly	Thr	Gly	Gln
				125					130					135
Thr	Ser	Ala	Glu	Leu	Glu	Val	Gln	Arg	Arg	His	Ser	Leu	Val	Ser
				140					145					150
Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp	Phe	Val	Gly	Val
				155					160					165

Asp Ser Leu Asp	Leu Cys Asp Gly Asp	Arg Trp Arg Glu Gln Ala	
170	175	180	
Ala Leu Asp Leu	Tyr Pro Tyr Asp Ala	Gly Thr Asp Ser Gly Phe	
185	190	195	
Thr Phe Ser Ser	Pro Asn Phe Ala Thr	Ile Pro Gln Asp Thr Val	
200	205	210	
Thr Glu Ile Thr	Ser Ser Ser Pro Ser	His Pro Ala Asn Ser Phe	
215	220	225	
Tyr Tyr Pro Arg	Leu Lys Ala Leu Pro	Pro Ile Ala Arg Val Thr	
230	235	240	
Leu Leu Arg Leu	Arg Gln Ser Pro Arg	Ala Phe Ile Pro Pro Ala	
245	250	255	
Pro Val Leu Pro	Ser Arg Asp Asn Glu	Ile Val Asp Ser Ala Ser	
260	265	270	
Val Pro Glu Thr	Pro Leu Asp Cys Glu	Val Ser Leu Trp Ser Ser	
275	280	285	
Trp Gly Leu Cys	Gly Gly His Cys Gly	Arg Leu Gly Thr Lys Ser	
290	295	300	
Arg Thr Arg Tyr	Val Arg Val Gln Pro	Ala Asn Asn Gly Ser Pro	
305	310	315	
Cys Pro Glu Leu	Gln Glu Glu Ala Glu	Cys Val Pro Asp Asn Cys	
320	325	330	

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcaatgcc aggggaagag gg 22

<210> 238

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

caggatcgc tacgtccg 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
caacaccttc tctctcttc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
ccattatca gggacgaact cagcc 25

<210> 241
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ctaccacagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cgtcacacgt gtctgcggg atg 23

<210> 243
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
cagcccttc tctctcttc tcccacgtcc tatctgctc tc 42

<210> 244

<211> 1994
<212> DNA
<213> Homo sapiens

<400> 244

gggggggtcc gtgagggggt cctttgggca ggggtagtgt ttggtgtccc 50
tgtcttggtg gatattgaca aactgaagct ttctgcacc actggactta 100
aggaagagtg taactgtagg cggacagctt tagtggccgg ccggccgctc 150
tcctcccccg taaggagcag agtcttttgt actgaccaag atgagcaaca 200
tcacacaca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gttgagata ttgacataga gttgtggtcc aaagaagctc cttaaagcttg 300
cagaaatttt atccaaattt gtttggaagc ttattatgac aataccattt 350
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acagggagtg gtggagagtc tatctatgga gcgcattcca aagatgaatt 450
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agtatataac atgttgcgac tgcagaagt agacattgat gatgacgaaa 650
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agaggaggaa gtaaaagaaat tgaaacccaa aggcacaaaa aatttttagtt 800
tactttcatt tggagaggaa gctgaggaag aagaggagga agtaaatoga 850
gttagtcaga gcacgaaggg caaaagcaaa agtagtcatg acttgcttaa 900
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atgcaccaga tttagttgat gatggagaag atgaaagtgc agagcatgat 1000
gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgcaca 1050
aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag 1100
aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150
agacaattaa aacgggaact cttagcagca aaacaaaaaa aagtagaaaa 1200
tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gccctccag 1250
atggtgctgt tgccgaatac agaagagaaa agcaaaagta tgaagctttg 1300

aggaagcaac agtcaaagaa gggaacttcc ogggaagatc agacccttgc 1350
 actggtgaac cagtttbaat ctaaactcac tcaagcaatt gctgaaacac 1400
 ctgaaatga cattcctgaa acagaagtag aagatgatga aggatggatg 1450
 tcaatgttac ttcagtttga ggataaaaagc agaaaagtga aagatgcaag 1500
 catgcaagac tcagatacat ttgaaatcta tgatcctcgg aatccagtga 1550
 ata caagaag gaggggaagaa agcaaaaagc tgatggagaga gaaaaaagaa 1600
 agaagataaa atgagaataa tgataaccag aacttgcttg aaatgtgcct 1650
 acaatggcct tgtaacagcc attgttccca acagatcac ttaggggtgt 1700
 gaagagaagt atttttgaac ctgttgtctg gttttgaaaa acaattatct 1750
 tgtttgcaa attgtggaat gatgtaagca aatgcctttg gttactggta 1800
 catctgtttt ttctagtctg accttttata ttgctaatc tgaataaaaa 1850
 taactttcct tcacacaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245
 <211> 472
 <212> PRT
 <213> Homo sapiens

<400> 245
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 1 5 10 15
 Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser
 20 25 30
 Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu
 35 40 45
 Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly
 50 55 60
 Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly
 65 70 75
 Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg
 80 85 90
 Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly
 95 100 105
 Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala
 110 115 120
 Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly
 125 130 135

Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu	395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met
455 460 465

Arg Glu Lys Lys Glu Arg Arg
470

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<270>

<213> Synthetic oligonucleotide probe

<400> 146

ctactggcac aggg 24

<210> 147

<211> 18

<212> DNA

<213> Artificial Sequence

<270>

<213> Synthetic oligonucleotide probe

<400> 147

agagttagtc agagcatg 18

<210> 148

<211> 18

<212> DNA

<213> Artificial Sequence

<270>

<213> Synthetic oligonucleotide probe

<400> 148

agagatggtgc tgttgccg 18

<210> 149

<211> 19

<212> DNA

<213> Artificial Sequence

<270>

<213> Synthetic oligonucleotide probe

<400> 149

caactggaac aggaactgag atgtggatc 29

<210> 250

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 150
ctctttcagc agtgcaaggg tctg 24

<210> 151
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 151
ctcttcgat taaaacgc 18

<210> 152
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 152
cagggactg gttgccatg caaatgttg ttctcatgat aatgg 45

<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

<400> 253
cgccgcggtt ggggctggaa gttcccgcca ggtccgtgcc gggcgagaga 50
gatgctgccc ggcccgcctc ggctttgagg cgagagaagt gtcccagacc 100
catttcgcct tgcctgacggc gtccagacct ggccagacat gtccacaggg 150
ttctcttcgc ggtccgggac tctgggctcc accaccgtgg ccgcggcgcg 200
gacacacaca ggcggcggttt tctccttcgg aacgggaacg tctagcaacc 250
cttctgtggg gctcaatttt ggaaatcttg gaagtacttc aatccagca 300
actacatctg ctccctcaag tggttttgga accgggctct ttggatctaa 350
acctgcactc gggttcactc taggaggaac aaatacaggt gccttgcaac 400
ccatgaggcc tcaagtggtc accaaatatg gaacctgca aggaaaacag 450
atgcattgtg ggaagacacc catccaagtc tttttaggag tccccttctc 500

cagacctcct ctagggtatcc tcaggtttgc acctccagaa cccccggagc 550
cctggaaaagg aatcagagat gctaccactt acccgccctgg atggagtctc 600
gctctgtcgc caggctggag tgcagtggca ccatctcggc tcactgcaac 650
ctccgctcc cgggttcaag caggtctcct gctcagcct ctgagtgtct 700
ggggtacag gtgcctgcag gagtccctggg gccagctggc ctgatgtac 750
ctcagcagc gggaaaggta caagtggctg cgttccagcg aggactgtct 800
gtacctgaac gtgtacgcgc cggcgcgcgc gcccggggat cccagctgc 850
cagtcatggt ctggttcccg ggaggccct tcatctggg cgtgtttct 900
tcgtacgagg gctctgattt ggcgcgcgc gagaaagtgg tgcgtgtgtt 950
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gttcggccag tcggcggggg ccatgagcat ctccaggactg atgatgtac 1150
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gctgagggc actatcagg accaaggtga tgcgtgtgtc caacaagatg 1350
agattcctcc aactgaactt ccagagagac ccggaagaga ttatctggtc 1400
catgacctt gtggtggatg gtgtggtgat cccagatgac cctttggtgc 1450
tctgacca cgggaaggtt tcatctgtgc cctaccttct aggtgtcaac 1500
aacctggaat tcaattggct cttgccttat aatatacca aggagcaggt 1550
accaattgtg gtggaggagt acctggacaa tgtcaatgag catgactgga 1600
agatgctacg aaaccgtatg atggacatag ttcaagatgc cactttcgtg 1650
tatgcacac tgcagactgc tcaataccac cgagaaacc caatgatggg 1700
aatctgcct gctggccacg ctacaacaag gatgaaaagt acctgcagct 1750
ggattttacc acaagagtgg gcatgaagct caaggagaag aagatggctt 1800
tttgatgag tctgtaccag tctcaaagac ctgagaagca gaggcaattc 1850
taagggtggc tatgcaggaa ggagccaaag aggggtttgc cccaccatc 1900

ccttccctgg ggagactagc catggacata cctggggaca agagttctac 1950
 caaccccagt ttagaactgc aggagctccc tgcctgctcc aggccaaaagc 2000
 t tgcctttt gccctgtgtg tgggaactgc actgcccctt ccagcctgac 2050
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 ctgtcaaac cacactgtgc tcaactctcc agctcagga caacctcttt 2150
 ttttcccttc ttcaaatct ccaccccttc aatgtctct tgtgactct 2200
 ccttatggga ggtcgacca gactgcact gccctgtca ctgcaaccag 2250
 cttagcattt accatccatc ctgtcaanc ttgtctctgt ctgttccat 2300
 tggcctggag gcctagggca ggtgtgaca tggagcaaac ttttggtagt 2350
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 ctctatacc aggggtggtc tcttcaata agaagtgttg attagaaaa 2450
 aaaaaa 2456

<210> 254
 <211> 545
 <212> PRT
 <213> Homo sapiens

<400> 254
 Met Ser Thr Gly Phe Ser Phe Gly Ser Gly Thr Leu Gly Ser Thr
 1 5 10 15
 Thr Val Ala Ala Gly Gly Thr Ser Thr Gly Gly Val Phe Ser Phe
 20 25 30
 Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly
 35 40 45
 Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser
 50 55 60
 Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly
 65 70 75
 Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg
 80 85 90
 Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
 95 100 105
 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe
 110 115 120
 Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro
 125 130 135

Pro	Ile	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	140	145	150
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	155	160	165
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	170	175	180
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	185	190	195
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	200	205	210
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	215	220	225
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	230	235	240
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	245	250	255
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Gln	Lys	Val	Val	Leu	Val	260	265	270
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	275	280	285
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	290	295	300
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	305	310	315
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	320	325	330
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	335	340	345
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	350	355	360
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	365	370	375
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	380	385	390
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	395	400	405
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	410	415	420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro		
	425	435
Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu		
	440	450
Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn		
	455	465
Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp		
	470	480
Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met		
	485	495
Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr		
	500	510
Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala		
	515	525
Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu		
	530	540
Pro Gln Glu Trp Ala		
	545	

<210> 255
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 255
 aggtgactgc aggagtcctg ggg 23

<210> 256
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 256
 ccacctcagg aagccgaaga tgcc 24

<210> 257
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 257

gaagggtaca agtgggtgog cttcagcgag gactgtetgt acctg 45

<210> 258

<1> 2764

<212> DNA

<213> Homo sapiens

<400> 258

gaqaacagge ctgtctcagg caggccctgc gccctctatg cggagatget 50
actgccactg ctgtctgctt cgtctgttgg cgggtcccag gctatggatg 100
ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150
tgcattcttg tgccctgctc tttctctac ccccgacaag actggacagg 200
gtctacccca gcttatggtt actggttcaa agcagtgaat gagacaacca 250
aggggtctct tgtggccaca aaccaccaga gtcgagaggt gjaatgagc 300
accgqgggct gattccagct cactggggat cccgccaaagg gjaactctc 350
cttggatgat agagaacgag agatgcagga tgaatcacag tactttcttc 400
gggttgagag aggaagctat gtgacatata atttcattgaa cgtatgggttc 450
ttctctaaaag taacagtgtt cagcttccag cccagaccac aggaccacaa 500
caccqacctc acctgccatg tggactcttc cagaaagggt gtgagcgcac 550
agagqacctt ccgactccgt gtggcctatg ccccagaga ccttggttatc 600
agcattctac gtgacaacac gcagccctg gaggccacag cccagggaaa 650
tgtcccatat ctggaagccc aaaaaggcca gttctctggg ctctctcttg 700
ctgttgacag ccagccccct gccacaatga gctgggtctt gcagaacaga 750
gtctctctct cgtcccatcc ctggggccct agaccctgg ggttgagct 800
gcccggggtg aaggctgggg attcagggtg ctacacctgc cagcgggaga 850
acaggcttgg ctccagcag cagccctgg acctctctgt gcagtatct 900
ccagajaaac tgagagtgat ggtttcccaa gcaaacagga cagtctgga 950
aaaccttggg aacggcacgt ctctccagt actggagggc caaagcctgt 1000
gcttggctg tgtcacacac agcagccccc cagccaggct gagctggacc 1050
cagaggggac aggtttctgag cccctccag cctcagacc cgggggtct 1100
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ctcggcacc actgggtctc cagcacgtct ctctcagcct ctccgtgcac 1200

tataagaagg gactcatctc aacggcattc tccaacggag cgtttctggg 1250
aatcggcattc acggctcttc ttttctctg cctggccctg atcatcatga 1300
agattctacc gaagagacgg actcagacag aaaccctcag gccacggctc 1350
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ccccctggct cagaagcgga atcagaaagc caccctaaac agtcctcgga 1450
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aagcagtatc agttgcccg tttccagaa cccaaatcat ccactcaagc 1550
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tcccaggcgt cagacccagg cctgagggcc gcatgcccaa ggcacccag 1650
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ctgggaactc ggetagggag gaaggtagag taagaggttg aagataacig 1750
agtgcacagt ttcttctct cctctctct ctctctttct ctctctctct 1800
ctctttctct ctcttttaaa aaaacatctg gccagggcac agtggctc 1850
gcctgtaatc ccagcacttt gggagggttg ggtgggcaga tcgctgagg 1900
tcgggagttc gagaccagcc tggccaactt ggtgaaaccc cgtctctact 1950
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tacttgggaa gctgaggcag gagaatcact tgaacctggg agacggaggt 2050
tgacgtgagc caagatcaca ccattgcacg ccagcctggg caacaaagg 2100
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cccagcactt tgggaggcta aggtgggttg attgcttgag cccaggagtt 2200
cgagaccagc ctgggcaaca tggtyaaac ccctctctac aaaaaataca 2250
aaacatagct gggcttggtg gtgtgtgct gtagtcccag ctgtcagaca 2300
tttaaaccag agcaactcca tctggaatag gagctgaata aaatgaggct 2350
gagacctact gggctgcatt ctacagacgt ggaggcattc taagtccag 2400
gatgagacag gaggtccgta caagatacag gtcataaaga ctttgctgat 2450
aaaacagatt gcagtaaaga agccaaccaa atcccaccaa aaccaagttg 2500
gccacgagag tgacctctgg tegtctcac tgtacactc ctgacagcac 2550
catgacagtt tacaaatgcc atggcaacat caggaagtta ccgatatgt 2600
cccaaaaggg ggaggaatga ataaccacc ccttgtttag caaataagca 2650

agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700
 ctatggagta gccattcttt tgttccttta cttctctaataa aaacttgett 2750
 tcaccttaaa aaaa 2764

<210> 259
 <211> 544
 <212> ERT
 <213> Homo sapiens

<400> 259
 Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln
 1 5 10 15
 Ala Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met
 20 25 30
 Val Pro Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr
 35 40 45
 Pro Arg Gln Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp
 50 55 60
 Phe Lys Ala Val Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr
 65 70 75
 Asn His Gln Ser Arg Glu Val Glu Met Ser Thr Arg Gly Arg Phe
 80 85 90
 Gln Leu Thr Gly Asp Pro Ala Lys Gly Asn Cys Ser Leu Val Ile
 95 100 105
 Arg Asp Ala Gln Met Gln Asp Glu Ser Gln Tyr Phe Phe Arg Val
 110 115 120
 Glu Arg Gly Ser Tyr Val Thr Tyr Asn Phe Met Asn Asp Gly Phe
 125 130 135
 Phe Leu Lys Val Thr Val Leu Ser Phe Thr Pro Arg Pro Gln Asp
 140 145 150
 His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly
 155 160 165
 Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro
 170 175 180
 Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu
 185 190 195
 Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys
 200 205 210
 Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro
 215 220 225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser	230	235	240
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val	245	250	255
Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala	320	325	329
Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn	455	460	465
Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu	500	505	510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg
515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu
530 535 540

Val Lys Phe Gln

<210> 160

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 160

caaaagctgc gcttggtctg tg 22

<210> 161

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 161

ttatgaagcc cagagggtgc tgag 24

<210> 162

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 162

ggagctgcca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 163

<211> 2857

<212> DNA

<213> Homo sapiens

<400> 163

tgaagagtaa tagttggaat caaaagagtc aacgcaatga actgttatatt 50

actgctgggt tttatgttgg gaattcctct cctatggcct tgtcttggag 100

caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtgggtg ggtgtggaac caattttttg taccagagga 200

aat taatacg actagtcato acatcggcca gctaagatct gatttagaca 250
atggaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
cttttatca ttgatgaag aacaggtgac atatatgcca tacagaagct 350
tcttagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400
tcttactgg aagggtctgt gaaactgagt ctgagtttgt catcaagtt 450
tcggatatca atgacaatga accaaaattc ctgatggaac cttatgaggc 500
cattgtacca gagatgtctc cagaagggaac attagttatc caggtgacag 550
caagtgatgc tgaogatccc tcaagtggta ataagtctcg tctctctac 600
agcttacttc aaggccagcc atattttctt gttgaaccaa caacaggagt 650
cataagaata tctttctaaa tggatagaga actgcaagat gagtattggg 700
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<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

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				20					25					30
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp
				35					40					45
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser
				50					55					60
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn
				65					70					75
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe
				80					85					90
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu
				95					100					105
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile
				110					115					120
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val
				125					130					135
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp
				140					145					150
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr
				155					160					165
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser
				170					175					180
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro
				185					190					195
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser
				200					205					210
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln
				215					220					225
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr
				230					235					240
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile
				245					250					255
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro
				260					265					270
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile
				275					280					285

Gly Glu Asn Ala	Glu Met Asp Tyr Ser	Ile Glu Glu Asp Asp Ser
290	295	300
Gln Thr Phe Asp	Ile Ile Thr Asn His	Glu Thr Gln Glu Gly Ile
305	310	315
Val Ile Leu Lys	Lys Lys Val Asp Phe	Glu His Gln Asn His Tyr
320	325	330
Gly Ile Arg Ala	Lys Val Lys Asn His	His Val Pro Glu Gln Leu
335	340	345
Met Lys Tyr His	Thr Glu Ala Ser Thr	Thr Phe Ile Lys Ile Gln
350	355	360
Val Glu Asp Val	Asp Glu Pro Pro Leu	Phe Leu Leu Pro Tyr Tyr
365	370	375
Val Phe Glu Val	Phe Glu Glu Thr Pro	Gln Gly Ser Phe Val Gly
380	385	390
Val Val Ser Ala	Thr Asp Pro Asp Asn	Arg Lys Ser Pro Ile Arg
395	400	405
Tyr Ser Ile Thr	Arg Ser Lys Val Phe	Asn Ile Asn Asp Asn Gly
410	415	420
Thr Ile Thr Thr	Ser Asn Ser Leu Asp	Arg Glu Ile Ser Ala Trp
425	430	435
Tyr Asn Leu Ser	Ile Phe Ala Thr Glu	Lys Tyr Asn Ile Glu Gln
440	445	450
Ile Ser Ser Ile	Pro Leu Tyr Val Gln	Val Leu Asn Ile Asn Asp
455	460	465
His Ala Pro Glu	Phe Ser Gln Tyr Tyr	Glu Thr Tyr Val Cys Glu
470	475	480
Asn Ala Gly Ser	Gly Gln Val Ile Gln	Thr Ile Ser Ala Val Asp
485	490	495
Arg Asp Glu Ser	Ile Glu Glu His His	Phe Tyr Phe Asn Leu Ser
500	505	510
Val Glu Asp Thr	Asn Asn Ser Ser Phe	Thr Ile Ile Asp Asn Gln
515	520	525
Asp Asn Thr Ala	Val Ile Leu Thr Asn	Arg Thr Gly Phe Asn Leu
530	535	540
Gln Glu Glu Pro	Val Phe Tyr Ile Ser	Ile Leu Ile Ala Asp Asn
545	550	555
Gly Ile Pro Ser	Leu Thr Ser Thr Asn	Thr Leu Thr Ile His Val
560	565	570

Cys Asp Cys Gly Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln	575	580	585
Glu Leu Val Leu Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala	590	595	600
Ile Leu Ile Cys Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr	605	610	615
Leu Gly Leu Lys Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys	620	625	630
Ser Glu Asp Phe Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly	635	640	645
Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg	650	655	660
Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser	665	670	675
Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro	680	685	690
Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu	695	700	705
Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr	710	715	720
Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser	725	730	735
Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu	740	745	750
Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly	755	760	765
Ser Ala Val Gln Ser Asn Asn	770		

<210> 265

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 24, 60, 141, 226, 228, 249, 252

<223> unknown base

<400> 265

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gaatattttt taaaatggat agagaactgc aagatgagta ttgggtaatc 100

attcagagca aggacatgat tggtcagaca ggggcgttgt ntggaacaa 150
aagtggtatta attaaacttt cagatgttaa tgacaataag cctatattta 200
aagaaagitt ataccgcttg actgtntntg aatctgcacc caatgggant 250
nttataggaa caatcatgjc atatgataat gacataggag agaatacaga 300
aatggattac agcaattgaag agpatgutte gcaaacattt gacattatt 349

<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg cacc 25

<210> 267

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aaatggttga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccacatcagg tccaggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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ccgccttaa cttcctccgc ggggccagc caccttcggg agtcggggtt 150

gcccacctgc aaactctcgc cctttctgcac ctgccacccc tgagccagcg 270
cgggcccccg agcgagtcac ggccaaacgc gggctgcagc tgttgggctt 280
ccttctcgcg ttcttgggat ggatcgggcg catcgtcagc actgccctgc 300
cccagtgagc gatttactcc tatgcgggcg acaacatcgt gaccgcccag 320
gcacatgacg aggggctgtg gatgtcctgc gtgtgcagc gcaccgggca 400
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<110> 270

<111> 211

<112> P&T

<113> Homo sapiens

<400> 270

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1				5					10					15

Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp

	20	25	30
Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala	35	40	45
Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly	50	55	60
Ile Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser	65	70	75
Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly Ile Leu Leu	80	85	90
Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met	95	100	105
Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val	110	115	120
Ile Gly Gly Ala Ile Phe Leu Leu Ala Gly Leu Ala Ile Leu Val	125	130	135
Ala Thr Ala Trp Tyr Gly Asn Arg Ile Val Gln Glu Phe Tyr Asp	140	145	150
Pro Met Thr Pro Val Asn Ala Arg Tyr Glu Phe Gly Gln Ala Leu	155	160	165
Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys Leu Leu Gly Gly Ala	170	175	180
Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Ser Tyr Pro Thr	185	190	195
Pro Arg Pro Tyr Pro Lys Pro Ala Pro Ser Ser Gly Lys Asp Tyr	200	205	210

Val

<210> 271

<211> 564

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 21, 69, 163, 434, 436, 444

<223> unknown base

<400> 271

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ggatggatcg ggcctatct cacaactgcc ttccccagtg gaggatttta 100

ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtaagagggg 150

ctgtggatgt ccnccgtgtc gcagagcacc ggcagatcc agtgcaaagt 200
 ctttgaactcc ttgctgaatc tgagcagcac attgcaagca acccgtgect 250
 tgaaggtagt tggcatccct ctgggagtga tagcaatctt tgtggccacc 300
 gtttgcctga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350
 gaggatgget gtcattgggg ggcgatatt tcttcttga ggtctggcta 400
 ttttagttgc cacagcatgg tatggcaata gaancttca acanttctat 450
 gacctatga cccagtcac tgcaggtaac gaatttggtc aggetctctt 500
 caatggctgg gctgctgctt ctctctgect tetgggaggt gccctacttt 550
 gctgttcttg tccc 564

<210> 272

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

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 tccagctgtt gggtctcatt ctcccttcc tgggatggac cggcgcccat 100
 cnttagcact gccctgccc agtggaggat ttactctat nccggnaca 150
 acatcgtgac cggccaggcc ntgtacgagg ggtgtggat gtctgctg 200
 tgcagagca cggggcagat ccagtcaaa gtctttgact ccttgctga 250
 atctgagcag cacattgcaa gcaaccctg ccttgatggt ggttggcatc 300
 ctctggggag tgatagcaat cttnntggcc accgttgtnn ntgaagtga 350
 tgaagtgtt ggaagacgat gaggtgcaga agatgaggat ggcgtgcatt 400
 gggggcgaga tatttctct tgcaggctctg gctattttag ttgccacagc 450
 atgctatggc aatagaatcg ttcaagaatt ctatgacct atgaccga 498

<410> 273

<411> 552

<412> DNA

<413> Homo sapiens

<420>

<421> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273

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atgagncgc gccatentca gactccctgc cccatggaga ttttncctat 100
gttggcgaca acatentgac ccccagccat gtaaggaggc ctttgaaagt 150
cngcgtgtcg cagancaccg ggcagatcca gtgcacagtc tttgactcct 200
tctgcatct gngcagcaca ttgcagcaac centgacctg atgctggttg 250
gcctcctcct gggagtgaata gcaatctttg tggccacctg tggcatgaag 300
tgtatgaagt gcttgggaaga ccatgaggtg cagaagatga ggcctgctgt 350
cattgggggc gcgatatttc ttcttgcagg tctggctatt tnnngttgac 400
acagctggt atggcaatg aatcgttcaa gaattctatg accctatgac 450
ccagctcaat gccaggtacg aatttggtca ggtctctctc actggtctgg 500
ctgctgttc tctctgctt ctgggaggtg cctactttg ctgttctgc 550
ga 550

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

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ccagtcaaaa gtctttgaat ccttgetgaa tctgagcagc acattgcaag 200
caaccctgtc cttgatgggg ttggcatcct cctgggagtg atagcaacct 250
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caggtctggc tatttttagt gccacagcat ggtatggcaa tagantntt 400
cnnnnntct atgacctat gacccacgtc aatgccaggt acgaatttgg 450

cttctctctc ttaactgget gggetgctgc ttctctctgc cttctgggaq 500
gtgactact ttgctgttcc tgtccc 525

<210> 275

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274

<223> unknown base

<210> 275

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gcacacacatt ncaagcaacc ccttgccctg aagggtggtg ncaccccccc 100

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ctgcttggga gaagatgagg tgcagaagat gaggatggct gtcattgggg 200

ggcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250

tatggcaata gnatnnttcg nggnttcctat gacctatga cccagtcac 300

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ctctctgctt tctgggaggt gcctacttt gctgttcctg cccccgaa 398

<210> 276

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476

<223> unknown base

<210> 276

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gagcagcaca ttgcaagcaa ccgtgcctt gatgggtggt ggcattcttc 200

tggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250

tgcttgggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300

cgggatattt ctntttgcag gtctggctat tttagttgac acagcatggt 350

atggcaatag aatngttcaa gaattttatg acctatgac cccagtcac 400

gdcaggtacg aatttggta ggtttnttc actggtggg ctgtgtcttn 450

tttttgcctt ntggggaggtg ccttantttg ctgttcttgc gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 133, 147, 163, 165-166, 172

<223> unknown base

<400> 277

ttctaggggg gcgcgatatt tttctttgca ggtntgggta ttttagttgc 50

caagcctgg tatggcaata gaatcgttca agaattntat gacctatga 100

ccacagtcac tgcaggtac gaatttgggc aggcctctntt cactggntgg 150

gcttctgctt ctntnngcct tntgggaggt gcctacttt gctgttcttg 190

<410> 278

<411> 542

<412> DNA

<413> Homo sapiens

<420>

<421> unsure

<422> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<423> unknown base

<400> 278

ttcttgggat ggatccggcc ccatcttcac atgccttgc cctgggagat 50

ttacacctat gctggcgaac aacatcttga ccgcccaggc catgtaagag 100

gggtgttggc atgtcttggc tgtcccagag caccggggcag atccagtcca 150

aagtctttga ctcttctgtg aatctgagca gcacatttga agcaaccttg 200

ccttgatggc ggttggcacc ctcttgggag tgatagcaat ctttgtggcc 250

accgttggca tgaagtgtc tgaagtgcct ggaagaagat gaggtgcaga 300

agatgaggat ggctgtcatt gggggcgoga tatttcttct tgcaggtctg 350

gctattttag nngccacagc atggtatggc aatcagaacc nntcanaaac 400

tctatgaacc tatgaaccca gtcaatgcca ggtacgaatt tggtcaggct 450

ctcttcaactg gctgggctgc tgcctctctc tgccttcttg gaggtgcct 500

actttgctgt tctgtcccc gaaaaacaac ctcttaccca cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
gggggtgca gctgttgggc ttcattctgc ttcctgggat ggaatcggcg 50
ccatgtcag cactgccttg ccccatggag gatttactcn tatgctggcg 100
ttacatcgt gacncccgag gccatgtacg aggggctgtg gatgtcngcg 150
tctcgagag caccgggcag atccagtga aagtctttga ctcttctgtg 200
tacttgga gacattgca agcaacntg ccttgatggg ggttggcact 250
ctcttggag tgatagcaat ctttgtggc accgttggca tgaagtgtat 300
gagtgtttg gaagacgat aggtgcagaa gatgaggatg gctgtcattg 350
ggggcagat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400
atggtatggc aatagaatcg tccaagaatt ctatgacct atgaccccag 450
tcattccag gtacgaattt ggtcaggctc tcttcaactgg ctgggctgct 500
ttctctctt gccttctggg aggtgcccta ctttctgttt cctgcgaa 548

<210> 130
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
cgagccagtc atggccaacg c 21

<210> 181
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 281
gtatcacacg tagtctttcc cgtctg 26

<210> 182
<211> 43

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 282
ctgcagatgt tgggttcat tctgccttc ctgggatgga tct 43

<210> 283
<211> 2785
<212> DNA
<213> Homo sapiens

<400> 283
ccgtgcctgc agctgcctgg gcacgcgggc ctgcctctg ccttcctccc 50
ctgcctctgc accgcctaga ccgaccccc cctccagcgc gccacccgg 100
tagaggcccc ccgcctgtgc ccgacccgt cccgccttt ttgtaaaact 150
taaagccggc gcagcattaa cgttccccc ccggtgacc tctcaggggt 200
ctcccccca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250
ggtcctgagc ctgcagccgc agcagagct csaattccga ggtcccttca 300
ccgatgttgt caccaccaac cttaaagcttg gcaaccgcac agaccgaaat 350
gtgtgtttta aggtgaagac tacagacca cgtaggtact gtgtgaggcc 400
caacagcgga atcatgatg caggggcctc aattaatgta tctgtgatgt 450
tacagccttt cgattatgat ccaatgaga aaagtaaaca caagtttatg 500
gttcagttta tgtttgctcc aactgacaat tcagatatgg aagcagtatg 550
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600
ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650
attatatcca caactgcac aaagacagaa acaccaatag tgtctaagtc 700
tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750
gtaagaggct gcaaggtgaa gttcagagc tacgggagga gaacaagcag 800
ttcaagggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850
ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcacc 900
ggctcttggc tctgggtggt ttgtttttta tcttggtgt aattattggg 950
aagattgact tctagaggta gcatgcacag gatggtaaat tggattggtg 1000
gaccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050

aattaatgta tgatgacatc tcacaggtct tgcctttaaa ttaccccttc 1100
 ctgacacac atacacagat acacacacac aaatataatg taacgatctt 1150
 ttgaaagtt aaaaatgtat agtaactgat tgagggggaa aaagaaatgat 1200
 ttttttaatt gaaaaggga accaatagta atgcacaaat ggcataattg 1250
 aatataatt tttaacattg ataggccttg gtacatgata ctgattaac 1300
 tctcttaaaa tgcacacctt cctgcctgtt tggctgtggt ccttggggag 1350
 ctggagcaca gaatgetygg gagtgcgttc agctcacac agtaagtcctc 1400
 atctgcaca ctcccgccc aggtgcttt cagtgtcttc agttctgttc 1450
 aaatcacaag ctcttggga ctgatcaca gagt tgaag cccaaaggaa 1500
 tttaactgtg gaagcaccag acgtactcgt tataagtga aggtgtgtgt 1550
 tgaatgattg acccagcgt ttggaaata atggcgtgc tttgttcaat 1600
 taagggaac agctaatt ttatattgtt catgtagtga agtcaaatg 1650
 ttttcagag atgtttaatg catatttaa ttatttaatg tatttcact 1700
 catgttttct tattgtcaca agagtacagt taatgetggt tgetgctgaa 1750
 ctctgttggg tgaactggta ttgtctgtg agggctgtgg gctcctctgt 1800
 ctctggagag tctggtcatg tggaggtggg gtttatttgg atgtggaga 1850
 agagtgcac ggaagtgtt ttcttgggt agtaataac aactgtcata 1900
 gggagggaat ttctcagtag tgacagtcaa ctctagggtt ctttttttaa 1950
 tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000
 actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050
 ggacctagcc tggagtcagg acaaatggat cgggctgcag agggttagaa 2100
 gogagggcac cagcagttgt gggtagggag caagggaaga gagaaactct 2150
 tcagcgaatc cttctagtag tagttgagag tttagctgtg aattaatttt 2200
 atgccataaa agaccaacc agttctgttt gactatgtag catcttgaaa 2250
 agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

1	5	10	15
Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu	20	25	30
Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys	35	40	45
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile	50	55	60
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro	65	70	75
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val	80	85	90
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val	95	100	105
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg	110	115	120
Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val	125	130	135
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr	140	145	150
Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu	155	160	165
Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val	170	175	180
Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly	185	190	195
Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala	200	205	210
Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu	215	220	225
Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys	230	235	240
Ile Ala Leu			

<210> 285

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255

<223> unknown base

<400> 285

atcagtccttc tagattgtcc ttatcccaac ttccaaccan tactaacatt 50
tcnagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100
ctggcgtcag gacaatggnt cgggctgcag aggnctagaa cgcagggcac 150
cagcagtttt gggctggggag caaggggnga gagaaactct tcagcgaate 200
cttctagtac tagttgagag ttgactgtg aattaatttt atgcacataa 250
agacnaacc agttctgttt gactatgtag catcttgaaa agaaaatta 300
tcataagcc ccaaaattaa gaattcttt gtcattttgt cacatttgc 350
ctatggggg aattattatt ttatcatttt tattatttg ccattggaag 400
gttaacttta aaatgagc 413

<210> 286

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 73, 97

<223> unknown base

<400> 236

tattgtaaag gccattttta accattggta ggccttggtt catgatgctg 50
gattacctcc ttaaattgaa ccttccctcg cctgttggtg ctggccnttg 100
gggagctgga gccccagcat gctggggagt ggggtcagct ccacacagta 150
gtccccagct ggcaccctcc cggcccagga tgctttccgt gtcttcagtt 200
ctgtccaaag catcagctcc ttgggaactga tgaacagagt cagaagccca 250
aaggaattgc cactgtggca gcacagagc tactcgtcat aagtgagagg 300
cgtgctttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350
gttcaactta agggaccaag ctaaattgta ttggttcatg tagtgaagtc 400
aaaetgttat tcagagatgt ttaatgcata ttaacttat ttaatgtatt 450
tcattccatg tttctattt gtcacaagag tacagttaat gctgcgtgct 500
gctgaactct gttgggtgaa ctgggtattg tgcctgaggg ctg 543

<210> 287

<211> 270

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 64, 72, 164, 198, 200, 220, 222, 223, 242

<223> unknown base

<400> 287

ccctgggtggg tttgtttcttt aattcggttg tgtaattttt ggggaagattg 50

ttttataggg tagmatgcac cnggctatga aattagattg gtggatccac 100

catctccatg agattitaaat ttatcatatc catgtatata aagaatttaa 150

tatctgatga catntcacag gtattgcttt taatttaccg atccctgnan 200

acaatataac agatccacac anacaaatnt aatgtaacga tnttttagaa 250

agtaaaaat gtatagttaa 270

<210> 283

<211> 423

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base

<400> 233

ggtagcccat tcccggccca ggcctgcttc cggtnttcag ttctgtccaa 50

gcctacagct ccttgggaact gatgaacaga gtcagaagcc caaaggaatt 100

gcactgtggg agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150

actgattgac ccagcgccttt ggaaataaat gccagtgctt tgttcantta 200

aaggagccaa gctaaaatttg tattgggttca tgtagtgaag tcaaactgtt 250

attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300

tggtttctta ttgtccaaag agtacagtta atgctgcgtg ctgctgaant 350

ntggttgggtg aactgggtatt gctgctggag ggctgtgggc tctctgtct 400

ttggagagtc tggatcatgtg gaggtggg 425

<210> 289

<211> 320

<212> DNA

<213> Homo sapiens

<400> 289

tgctttccgt gtcttcagtt ctgtccaaag cctcagctcc ttgggaactg 50

atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100
 tactegtcac aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150
 gaaataaatg gcagtgcctt gttaacttaa agggaccaag ctaaatttgt 200
 attgggtcac gtagtgaagt caaactgtta ttcagagatg tttaatgcac 250
 atttaactta tttaatgtat ttcatctcat gttttcttat tgtaacaaga 300
 gtacagttaa tgctgggtgc 320

<210> 220

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
 447, 481, 513, 532, 584, 598

<223> unknown base

<400> 220

aaacatttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50
 gaaacattgn gtaatgccac aatggcatat tgtaaatgtc attttaaaac 100
 ctgtatggcc ttggtacatg atgtctggatt acctctctta aaatgacacc 150
 ctctctggcc tgttggtgtc ggccttggg gagctngagc ccagcatgct 200
 gggtaagtcg gtctgtctca cacagtatgc cccangtggc ccantcccg 250
 cccnggtgtc ttccgtgtc ttcagttctg tccaagccat cagctccttg 300
 ggantgatga acagagtcag aagcccaaaag gaattgcant gtggcagcat 350
 cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaaccagc 400
 gctttgaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450
 atttgtattg gtccatgtag tgaagtcaaa ntgttattca gagatgttta 500
 atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550
 acaagggtac agttaatgct gcgtgtctgt gaantctgtt gggatgaantg 600
 gtattgtgtg 609

<410> 221

<411> 493

<412> DNA

<413> Homo sapiens

<400> 221

ggccttggg gagctggagc ccagcatgct ggggagtgcg gtcagctcca 50
 cactagtagc cccacgtggc ccactcccgg cccaggetgc tttccgtgtc 100
 ttcagttctg tccaagccat cagctccttg ggactgatga acagajtcag 150
 aagcccaaaag gaattgcact gtggcagcat cagaectact cgtcataagt 200
 gagaggcgtg tgttgactga ttgaccagc gctttggaaa taaatggcag 250
 tgccttggtc acttaaaggg accaagctaa atttgattg gtccatgtag 300
 tgaagcaaa ctgttattca gagatgttta atgcataatt aacttattta 350
 atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400
 ggggtgtgct gaactctgtt ggggtgaactg gtattgctgc tggagggctg 450
 tgggtccctc tgtctctgga gagtctggtc atgtggaggt ggg 493

<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gaccacgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccacaga gccaaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

caacgggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

tggagctccg ggtgctgtgg ccgggccttg ggggggcggc ctccggtcca 50
 tgggtgtga gaggtcccca gctgcagcgt cccgcccgc ctctcggga 100
 gctctgatct cagctgacag tgcctcggg gacnaaaca gctggcagg 150
 ctctcacttt gttgcccagg ctgaggttca gtgccttcat catgggtttac 200
 tgaagccttg acctcctggg ttcaagcga cctgctgagt agctgggaact 250
 ccaggacaaa attagaagat caaatggaa aatatgctgc tttggttgat 300
 atttttcacc cctgggtgga ccttcattga tggatctgaa atggaatggg 350
 attttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400
 ttccatctca ccagcccccg atttgaggca gatgctaaga tgatggtaaa 450
 tacagtgtgt ggcctcgaat gccagaaaga actcccaact cccagccttt 500
 ctgaattgga ggattatctt tcttatgaga ctgtctttga gaatggcacc 550
 cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600
 aaatatcacc acaaagggag tatctgttag gagaaagaga caggtgtatg 650
 gcaccgacag caggttcagc atcttggaca aaaggttctt aaccaatttc 700
 cctttcagca cagctgtgaa gctttccacg ggtgttagtg gcattctcat 750
 ttccctcag catgtttctaa ctgctgcaca ctgtgttcat gatggaaagg 800
 actatgtcaa agggagtaaa aagctaaggg taggggtgtt gaagatgagg 850
 aataaaaagtg gaggcaagaa acgtcgaggt tctaagagga gcaggagaga 900
 agctagtggg ggtgacaaaa gagagggtao cagagagcat ctgcaggaga 950
 gagogaaggg tgggagaaga agaaaaaat ctggccgggg tcagaggatt 1000
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 tcogaagggc tgggcacgag gaggcctggg ggaagctacc ttgactatg 1100
 actatgctct tctggagctg aagcgtgctc acaaaaagaa ataatggaa 1150
 cttggaatca gcccaacgat caagaaaatg cctgggtggaa tgatccaatt 1200
 ctccaggattt gataacgata gggctgatca gttgggtctat cggttttgca 1250
 gtgtgtccga cgaatccaat gatctccttt accaatactg cgatgctgag 1300
 tcgggctcca ccgggttcggg ggtctatctg cgtctgaaag atccagacaa 1350
 aaagaattgg aagcgcaaaa tcattcggtt ctactcaggg caccagtggg 1400

tggatgtcca cgggggttcag aaggactaca acgttgetgt togcataact 1450
 ccactaanat acgccagat ttgcctctgg attcaaggga acgatgcaaa 1500
 ttgtgcttac ggctaacaga gacctgaaac agggcggtgt atcatctaaa 1550
 tccagagaaa aaccagctct gcttaccgta gtgagatcac ttcataggtt 1600
 atgcctggac ttgaactctg tcaatageat ttcaacattt tcaaaaatca 1650
 ggagattttc gtccatttaa aaaatgtata ggtgcagata ttgaaactag 1700
 gtgggcactt caatgccaag tatatactct tctttacatg gtgatgagtt 1750
 tcatttgtag aaaaattttg ttgccttctt aaaaattaga cacaatttaa 1800
 accttcaaac aggtattata aataacatgt gactccttaa tggacttatt 1850
 ctccgggtcc tactcttnga agaatctaat aggatgctgg ttgtgtatta 1900
 aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950
 atagagacag aaagttacaa cacagtttgt actactctga gatggatcca 2000
 ttccagctcat gccctcaatg tttatatgtt gttatctgtt gggctctggga 2050
 catttagttt agtttttttg aagaattaca aatcagaaga aaaagcaagc 2100
 attataaaca aaactaataa ctgttttact gctttaagaa ataacaatta 2150
 caatgtgtat tatttaaaaa tgggagaaat agtttggtct atgaaataaa 2200
 cctagtttag aaatagggaa gctgagacat ttttaagatct caagttttta 2250
 ttttaactaat actcaaaata tggacttttc atgtatgcac agggaagaca 2300
 cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350
 atacattcta tgtatgaggt gctacatttt taggacaaaag aattctgtaa 2400
 tctttttcaa gaaagagctt tttctcctt gacaaaatcc agcttttgta 2450
 tgaggactat aggggtgaatt ctctgattag taattttaga tatgtccttt 2500
 cctaaaaatg aataaaattt atgaatatga 2530

<110> 296

<111> 413

<112> PET

<113> Homo sapiens

<100> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp
1				5				10					15	

Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His

	29	35	40
Leu Arg Lys Val	Pro Arg Ile Val	Ser Glu Arg Thr Phe His	Leu
	35	40	45
Thr Ser Pro Ala	Phe Glu Ala Asp Ala	Lys Met Met Val Asn Thr	
	50	55	60
Val Cys Gly Ile	Glu Cys Gln Lys Glu	Leu Pro Thr Pro Ser	Leu
	65	70	75
Ser Glu Leu Glu	Asp Tyr Leu Ser Tyr	Glu Thr Val Phe Glu	Asn
	80	85	90
Gly Thr Arg Thr	Leu Thr Arg Val Lys	Val Gln Asp Leu Val	Leu
	95	100	105
Glu Pro Thr Gln	Asn Ile Thr Thr Lys	Gly Val Ser Val Arg	Arg
	110	115	120
Lys Arg Gln Val	Tyr Gly Thr Asp Ser	Arg Phe Ser Ile Leu	Asp
	125	130	135
Lys Arg Phe Leu	Thr Asn Phe Pro Phe	Ser Thr Ala Val Lys	Leu
	140	145	150
Ser Thr Gly Cys	Ser Gly Ile Leu Ile	Ser Pro Gln His Val	Leu
	155	160	165
Thr Ala Ala His	Cys Val His Asp Gly	Lys Asp Tyr Val Lys	Gly
	170	175	180
Ser Lys Lys Leu	Arg Val Gly Leu Leu	Lys Met Arg Asn Lys	Ser
	185	190	195
Gly Gly Lys Lys	Arg Arg Gly Ser Lys	Arg Ser Arg Arg Glu	Ala
	200	205	210
Ser Gly Gly Asp	Gln Arg Glu Gly Thr	Arg Glu His Leu Gln	Glu
	215	220	225
Arg Ala Lys Gly	Gly Arg Arg Arg Lys	Lys Ser Gly Arg Gly	Gln
	230	235	240
Arg Ile Ala Glu	Gly Arg Pro Ser Phe	Gln Trp Thr Arg Val	Lys
	245	250	255
Asn Thr His Ile	Pro Lys Gly Trp Ala	Arg Gly Gly Met Gly	Asp
	260	265	270
Ala Thr Leu Asp	Tyr Asp Tyr Ala Leu	Leu Glu Leu Lys Arg	Ala
	275	280	285
His Lys Lys Lys	Tyr Met Glu Leu Gly	Ile Ser Pro Thr Ile	Lys
	290	295	300
Lys Met Pro Gly	Gly Gly Met Ile His	Phe Ser Gly Phe Asp	Asn Asp

305	310	315
Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu		
320	325	330
Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser		
335	340	345
Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys		
350	355	360
Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp		
365	370	375
Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg		
380	385	390
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly		
395	400	405
Val Asp Ala Asn Cys Ala Tyr Gly		
410		

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

ccatctccag gagagagcga aggg 24

<210> 198

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 198

ccatcttccc gtgaatccag aggg 24

<210> 199

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 199

gaaggaaggg cttcctttca gtggaccgg gtcaagaata cccac 45

<210> 300

<211> 1869

<212> DNA

<213> Homo sapiens

400> 300

aatgtgagag ggggtgatgg aagetgatag gcaggactgg agtgttagca 50
ccagtactgg atgtgacagc aggcagagga gcaattagca gcttattcag 100
tgtccgattc tgattccggc aaggatccaa gcatgggaatg ctgcgcctgg 150
gcaactcctg gcacactgat cctctttctg gctttccctg ccttgagttc 200
caggacccga cgtcccgagg aggacccgga cggcctatgg gatgcctggg 250
gcacatggag tgaatgctca cgcacctgag ggggaggggc ctctactct 300
ctgaggcgct gcttgagcag caagagctgt gaaaggaaga atatccgata 350
cagaacatgc agtaatgttg actgcacacc agaagcaggt gatttccgag 400
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gaatggcttc ctgtgtctaa tgacctgac aacctatgtt cactcaagt 500
ccaagccaaa ggaacaaacc tggttgttga actagcaact aaggtcttag 550
atggtacggg ttgctataca gaatctttgg atatgtgcac cagtgggtta 600
tgccaaattg ttggtcgga tcaacagctg ggaagcaccg tcaaggaa 650
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tcacttatat ctggaaaaca aaacctcca ggggaactaaa ggtgaaaaca 850
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gatccttgtc cagccagtga cggatacaag cagatcatgc cttatgacct 1250
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 ccttaagatg ccacatgggc agccttgcaa cttttttgac tgcctaaat 145
 ggcaggcaca ggagtgtct cctgtcacag tgcattgttg ccagggcctc 150
 agataccgtg ttgtctcttg catcgaccat caggaatgc acacaggagg 155
 ctgtagccca aaaacnagc ccacataaaa agaggaatgc atcgtaccca 160
 ctccctgcta taaacccaaa gagaaacttc cagtccagggc caagttgcca 165
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 gccctcgtaa gttgtaaaag cacagactgt tctatatttg aaactgtttt 175
 gtttaagaa agcagtgtct cactggttgt agctttcatg ggtttctaac 180
 taagtgtaat cctctacca aagctttttg gctctcaaat taaagattga 185
 ttactttcaa aaaaaaaa 186

<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

Met	Glu	Cys	Cys	Arg	Arg	Ala	Thr	Pro	Gly	Thr	Leu	Leu	Leu	Phe
1				5					10					15
Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu
				20					25					30
Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
				35					40					45
Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys
				50					55					60
Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr
				65					70					75
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala
				80					85					90
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe
				95					100					105
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser
				110					115					120
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala
				125					130					135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly	305	310	315
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro	350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His	365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser	380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu	395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys	410	415	420

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe
				425					430					435
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val
				440					445					450
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp
				455					460					465
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro
				470					475					480
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro
				485					490					495
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln
				500					505					510
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser
				515					520					525

<210> 302

<211> 1533

<212> INA

<213> Homo sapiens

<400> 302

cggaacgcgtg ggaggcggtt ggggaactcc cgtggagggg ccggtgggccc 50

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ctggggcggg cgtctgtggt ggcgccccc cgttcgttg ggcccagggt 150

ccagcggtg ccagaggcg gggaccccg cctcatgcac gggaagaactg 200

tgtgatcac cggggcgaa acgggccttg gcgcggccac ggccggcgag 250

ctaactggcc tgggagcgcg ggtgatcatg ggctgcgggg accgcgcgcg 300

cgcggaggag ggggggggtc agctccggcg cgagctccgc caggccggcg 350

agtgcggccc agagcctggc gtcagcgggg tggcgagct catagtcgg 400

gagctggacc tgcctcgtt ggcctcgtg ccgccttct gccaggaaat 450

gtccaggaa gagcctaggc tggatgtctt gatcaataac gcagggatct 500

tccagtggcc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550

gtgaaccata tggggcaatt tctactcac aatcttctcc ttggactcct 600

caaaagtcca gctccagca ggattgtgt agttttctcc aaactttata 650

aatacggaga catcaatttt gatgaattga acagtgaaca aagctataat 700

aaaagctttt gttatagccg gagcaaacgt gctaacatto tttttaccag 750

ggaactagcc cgcgcgttag aaggcacaaa tgcacccgtc aatgtgttgc 800
 atcctgggtat tglacggaca aatctgggga ggcacatata cattccactg 850
 ttgttcaaac cactcttcaa ttgtgtgtca tgggtttttt taaaaactcc 900
 actagaaggt gccacagcct ccatttatit ggcctcttca cctgaggttag 950
 aaggagtgtc aggaagatac ttgtgggatt gtaagagga agaactgttg 1000
 cccaaageta tggatgaac tgttgcaaga aaactctggg atatcagtga 1050
 agtgatgggt ggcctgtcaa aataggaaca aggagtuaaa gagctgttta 1100
 taaaactgca tatcagttat atctgtgac aggaatggtg tggattgaga 1150
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200
 ggtacatgtg ggtattttgg agttactgaa aaattatttt tgggataaga 1250
 gaatttcagc aaagatgttt taaatatata tagtangtat aatgaataat 1300
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
 tggatgacat attaatattt gtcagaatta agtgactcaa agtgcctatg 1400
 agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
 ttactacaat gtttgggtgt tgtgtggaaa ttatctgect ggtgtgtgca 1500
 cacaagtctt acttggataa aattttactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly
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Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln
			20					25					30	
Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr
			35					40					45	
Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala
			50					55					60	
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg
			65					70					75	
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu
			80					85					90	
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly

	95	100	105
Val Gly Glu Leu	Ile Val Arg Glu Leu	Asp Leu Ala Ser Leu Arg	
	110	115	120
Ser Val Arg Ala	Phe Cys Gln Glu Met	Leu Gln Glu Glu Pro Arg	
	125	130	135
Leu Asp Val Leu	Ile Asn Asn Ala Gly	Ile Phe Gln Cys Pro Tyr	
	140	145	150
Met Lys Thr Glu	Asp Gly Phe Glu Met	Gln Phe Gly Val Asn His	
	155	160	165
Leu Gly His Phe	Leu Leu Thr Asn Leu	Leu Leu Gly Leu Leu Lys	
	170	175	180
Ser Ser Ala Pro	Ser Arg Ile Val Val	Val Ser Ser Lys Leu Tyr	
	185	190	195
Lys Tyr Gly Asp	Ile Asn Phe Asp Asp	Leu Asn Ser Glu Gln Ser	
	200	205	210
Tyr Asn Lys Ser	Phe Cys Tyr Ser Arg	Ser Lys Leu Ala Asn Ile	
	215	220	225
Leu Phe Thr Arg	Glu Leu Ala Arg Arg	Leu Glu Gly Thr Asn Val	
	230	235	240
Thr Val Asn Val	Leu His Pro Gly Ile	Val Arg Thr Asn Leu Gly	
	245	250	255
Arg His Ile His	Ile Pro Leu Leu Val	Lys Pro Leu Phe Asn Leu	
	260	265	270
Val Ser Trp Ala	Phe Phe Lys Thr Pro	Val Glu Gly Ala Gln Thr	
	275	280	285
Ser Ile Tyr Leu	Ala Ser Ser Pro Glu	Val Glu Gly Val Ser Gly	
	290	295	300
Arg Tyr Phe Gly	Asp Cys Lys Glu Glu	Glu Leu Leu Pro Lys Ala	
	305	310	315
Met Asp Glu Ser	Val Ala Arg Lys Leu	Trp Asp Ile Ser Glu Val	
	320	325	330
Met Val Gly Leu	Leu Lys		
	335		

<210> 304

<211> 521

<212> EHA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 34, 62, 87, 221, 229

<223> unknown base

<400> 304

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gcaagaaaat tntgggatat cagtgaagtg atgggttngcc tgctaaaata 100
ggaacaagga gtaaaagagc tgtttataaa actgcataac agttatatct 150
gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagatt 250
actgaaaaat tatTTTTTggg ataagagaat ttcagcaaag atgttttaaa 300
tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
attotaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
gaattaagtg actcaaaagt ctatcgagag gtttttcaag tatctttgag 450
tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
tggaatttat ctgcctggct t 521

<210> 305

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 305

ccaggaatg ctccaggaag agcc 24

<210> 306

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 306

gacatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

aacgcagggga ttttccagtg cctttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

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cggagcccag ccttttecta acccaacca acctagccca gtcccagccg 100
ccagcgcctg tccctgtcac ggaccccagc gttaccatgc atcctgcctg 150
cttccatccc ttaccgcacc tcagatgctc ccttctgctc ctggtaactt 200
gggtttttac tccctgtaaca actgaaataa caagtcttgc tacagagaat 250
atagatgaaa ttttaaacaa tgcctgatgtt gctttagtaa atttttatgc 300
tgaactggtg cgttttcagtc agatgttgca tccaattttt gaggaagctt 350
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450
caataacca acctccaaat tgtttcgtaa tgggatgatg atgaagagag 500
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tggcgacaaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800
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gataaatgtg ttctctttgt ccgagaaata acatttgaaa atggagagga 900
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gaaagcaagc ccaagatgta gcaagcagtc caccatagag ctctttccag 1300
 caatagcac cctgttaata taggtatact ctattgagg atcagatatn 1350
 qtttlaaaaa ctgtgaaaaac agttttgtaag ctttttaaaa atagatataa 1400
 cctacgtggt ggaatagta aacctatatt ttctatattc tatgtgtatt 1450
 tttattttga ataacagaa agaatttta aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309
 <211> 406
 <212> PRT
 <213> Homo sapiens

<400> 309
 Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser
 1 5 10 15
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 20 25 30
 Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn
 35 40 45
 Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe
 50 55 60
 Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile
 65 70 75
 Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val
 80 85 90
 Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser
 95 100 105
 Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys
 110 115 120
 Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr
 125 130 135
 Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu
 140 145 150
 Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly
 155 160 165
 Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg
 170 175 180
 Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe
 185 190 195

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile	200	205	210
Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly	215	220	225
Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys	230	235	240
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu	245	250	255
Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys	260	265	270
Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg	275	280	285
Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp	290	295	300
Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro	305	310	315
Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr	320	325	330
Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys	335	340	345
Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe	350	355	360
His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala	365	370	375
Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu	380	385	390
Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu	395	400	405

Leu

<210> 310

<211> 182

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 36, 48

<223> unknown base

<400> 310

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 ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
 caacctcaca attgtttcgt aatgggatga tgatgaagag agaatacagg 150
 ggccagcgat cagtgaagc attggcagat ta 182

<210> 311

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 59, 140, 163, 174, 183, 282-283, 294-295, 319, 396

<223> unknown base

<400> 311

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 gagaggacna ggtgcgcgtg cctggagaat cctccgctgc cgtcggtcc 100
 agagcgccag ccccttctca acccaacca acctagccn gtcccagcg 150
 ccagcgcttg tccctgtcnc ggancccagc gtnaccatgc atcctgcgt 200
 cttctatccc ttacccgacc tcagatgtc cctctgtc ctggtaact 250
 gggtttttac tccgtgaaca actgaaataa cnggtcttga taennagaat 300
 atagatgaaa ttttaacna tctgatgtg gcttttagtca atttttatgc 350
 tgaactggtgt cgtttcagtc agatgtggca tccaatttt gaggangett 400
 ccgatgtcat taaggaagaa ttcccaatg aaaatcaagt agtgtttgcc 450
 agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500
 caaatacca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
 aatacagggg tcagcgatca gtgaaagcat tggcagatta catcagc 593

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

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<210> 313

<211> 19

<212> DNA

<212> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgcac agtgaaagc 19

<100> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccgcgaatgaa gtagctcggc 20

<100> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

ccgcactcaaa atgcattgtc 20

<100> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316

ccatttggcag gaattgtcc 19

<100> 317

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

cggtgctatag gccaaaggg 18

<100> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctctatctctt ggcttatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctctatctctt ttgcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

tgctttctta tctttaccgg acctcagatg ctcccttctg ctcttg 46

<210> 321

<211> 1533

<212> DNA

<213> Homo sapiens

<400> 321

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cgctgcctgc cactgcggcg ctcatctttct tggccatttg gcacattata 100
gcatttgcgt agctgaagac tgattacaag aatcctatag accagtgtaa 150
tacctgaat cccctgtgac tccagagta cctcatccac gctttcttct 200
gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250
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catattgtca gaaggaagga tggtgcaaat tagcttttta tcttttagca 400
tttttttaact acctatatgg catgatctat gttttgggtga gctcttagaa 450
caacacacag aagaattggg ccagtttaagt gcatgcacaaa agccacacaa 500
tgaaggcatt ctatccagca agatcctgtc caagagttag ctgtggaata 550
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ttttgccttgt ggaaagactg ttttccatag ttatactcag ataaagattt 650
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 caggtttgaa ctgcaacttc ttaaggaaca gcataatcc tctgaatgat 750
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800
 ctgttagggc tcatttttgg ttcattgaaa cagtatctaa ttataaatta 850
 actgtagata tcaggtgctt ctgatgaagt gaaaatgat atctgaactag 900
 tgggaaaact catgggttcc ctcatctgtc atgtcgatga ttatatatgg 950
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000
 tccctgtata ttgatgaat gagagatttc ccatatttc atcagagtaa 1050
 taaataract tgccttaatt cttaagcata agtaaactg atataaaaat 1100
 atatgctgaa ttacttgtga agaattgcatt taaagctatt ttaaatgtgt 1150
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200
 ttataatctg gtggtaaagg tattcttaag aatttcagc tactacagat 1250
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccctta 1300
 gtgaatata ataaaactct gaaattaaga ctg 1333

<210> 322

<211> 144

<212> PKT

<213> Homo sapiens

<400> 322

Met	Ala	Phe	Thr	Phe	Ala	Ala	Phe	Cys	Tyr	Met	Leu	Ala	Leu	Leu
1				5					10				15	
Leu	Thr	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala
				20					25				30	
Phe	Asp	Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys
				35					40				45	
Asn	Thr	Leu	Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Ile	His	Ala
				50					55				60	
Phe	Phe	Cys	Val	Met	Phe	Leu	Cys	Ala	Ala	Glu	Trp	Leu	Thr	Leu
				65					70				75	
Gly	Leu	Asn	Met	Pro	Leu	Leu	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Met
				80					85				90	
Ser	Arg	Pro	Val	Met	Ser	Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr
				95					100				105	

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser
140

<210> 323

<211> 4'7

<212> DNA

<213> Homo sapiens

<400> 323

attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50

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cttctgtctc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150

ctaggacct cttggcatat catatttggc ggtatatgag tagaccagt 200

ctgagtggcc caggactcta tgacctaca accatcatga atgcagatat 250

tctagcatat tgtcagaagg aaggatggtg caaattagct ttttatcttc 300

tgtatctttt ttactacctc tatggcatga tctatgtttt ggtgagctct 350

tatgacacac cacagaagaa ttggtccagt taagtgcctg caaaaagcca 400

caaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450

ggtctctatc agttaacttta aaaaatg 477

<210> 324

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 324

tgttaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 325

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
ctttagataga gtgggttaca 30

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
acttagacaa ttctttgtg 20

<210> 328
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gcatatttag catattgtca gaagggaagga tggtagaaaat tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
cggacgggtg ggggaaaacc ttccgagaaa acagcaacaa gctgagctgc 50
tgtgacagag gggaacaaga tggcgggccc gaaggggagc ctctgggtga 100
ggacccaact ggggtcccg ccgctgctgc tgcagaccat ggccttgccc 150
ggaggttcgg ggacgcttc ggcgaagca ttgactcgg tcttggtga 200
taagggtct tgcacggg cctgtcagtt gaactaccc ttgcacacct 250
acctaaagga agaggagttg taagcatgtc agagaggttg caggctgttt 300
tcaatttgc agtttgtgga tgatggaatt gaactaaac gaactaaatt 350
ggaatgtgaa tctgcattga cagaagcata ttcccaatct gatgagcaat 400
atgcttgcca tcttggttgc cagaatcagc tgcattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgcacaaa atgcacctac tctttccctct 500
 aactctgggtg aggtcattct ggagtgacat gatggactcc gcacagagct 550
 tcataacctc ttcattggaat ttttatcttc aagccgatga cggaaaaata 600
 gttatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650
 qgagcctaca aatttgagag aatcatctct aagcaaatg tcttatctgc 700
 aatgagaaaa ttcacaaggc cacaggaatt ttcttgaaga tggagaaagt 750
 gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800
 aactcttgtc ctctcgggtg tggatttgc ttggatttgc tgtgcaactg 850
 ttctacagc tgtggagcag tatgttccct ctgagaagct gattatctat 900
 ggtgaacttg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950
 ttctcttggtg gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000
 ctctacctac aaaagtgaat ctgtctcatt ctgaaattta agcatttttc 1050
 ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100
 ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150
 caantaaagt tactcaaac tctg 1174

<210> 330

<211> 323

<212> PFT

<213> Homo sapiens

<400> 330

Met	Ala	Ala	Pro	Lys	Gly	Ser	Leu	Trp	Val	Arg	Thr	Gln	Leu	Gly
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Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20						25				30	
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35						40				45	
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50						55				60	
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65						70				75	
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80						85				90	
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95						100				105	

Gln Ser Asp Glu Gln Tyr Ala Cys His	Leu Gly Cys Gln Asn Gln
110	115 120
Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met	
125	130 135
Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe	
140	145 150
Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser	
155	160 165
Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe	
170	175 180
Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu	
185	190 195
Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu	
200	205 210
Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly	
215	220 225
Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp	
230	235 240
Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp	
245	250 255
Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro	
260	265 270
Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu	
275	280 285
Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg	
290	295 300
Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys	
305	310 315
Val Asn Leu Ala His Ser Glu Ile	
320	

<210> 331

<211> 350

<212> DNA

<213> Homo sapiens

<400> 331

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gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100

ggctgttttc aatttgcag tttgtggatg atggaattga cttaaattcga 150

actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200
 tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgtg 250
 aactgagaca agaacaactt atgtccctga tgcacaaaat gcacctactc 300
 ttctctctaa ctctggtgag gtcattctgg agtgacatga tgaactccgc 350

<210> 332

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 47

<223> unknown base

<400> 332

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 aaacagcaac aagctgagct gctgtgacag agggacaacag atggcggcgc 100
 cgaaggcagc ctttgggtga ggacccaact ggggctcccg ccgtctgtgc 150
 tgcagacatc ggccctggcc ggaggttcgg ggaccgcttc ggcctgaagca 200
 ttctactcgg tcttgggtga taaggcgtct tgccacgggg cctgtcagtt 250
 gactatccc ttgcacacct accttaagga agaggagtgc taagcatgct 300
 agagagcttg caggtctgtt tcaatttgc agtttggtga tgatggaatt 350
 gactataatc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400
 ttcccatctc gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450
 tgcattccgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500
 atgcaactac tcttctctct aactctggtg aggtcattct ggagtgaatc 550
 gatggactcc gc 562

<210> 333

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 333

tcagctgag ctgctgtgac ag 22

<210> 334

<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 334
tgattetggc aaccaagatg gc 22

<210> 335
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 335
atggcttgg ccggagggtc ggggacgct tggctgaag 40

<210> 336
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 336
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ggcccgagg gtggggcgcc gtggggcgc gcccgcaagg gtttcattctg 100
agggcgcaag gcccgcgacc gagcgtgccc actggcctcc caagcgtggg 150
gggacaagct gccggagctg caatgggcgc cggctgggga ttcttgtttg 200
gcctcctggg cgcctgtgtg ctgctcagct cgggcacagg agaggagcag 250
cccccgga cagcggcaca gaggtgcttc tgcaggtta gtggttactt 300
ggatgattgt acctgtgatg ttgaaacct tgatagattt aataactaca 350
ggctttttcc aagaactaca aaacttcctg aaagtgaact ctttaggtat 400
tacaaggtaa acctgaagag gcctgtgctc ttctggaatg acatcagcca 450
gtgtggaaga agggactgtg ctgtcaaac atgtcaatct gatgaagttc 500
ctgatggaat taaatctggc agctacaagt attctgaaga agccaataat 550
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600
ctcagtgag gaaacacaga agcctgttct tcagtggacc aagcatgatg 650
attcttcaga taactctgtg gaagctgatg acattcagtc cctgaagct 700
gaatatgtag atttgcctct taatcctgag cgtacactg gttacaaggg 750
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr
20 25 30

Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp	35	40	45
Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg	50	55	60
Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg	65	70	75
Tyr Tyr Lys Val Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp	80	85	90
Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln	95	100	105
Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr	110	115	120
Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu	125	130	135
Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys	140	145	150
Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe	155	160	165
Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp	170	175	180
Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp	185	190	195
Ala Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys	200	205	210
Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln	215	220	225
Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu	230	235	240
Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His	245	250	255
Ala Ser Ile Asn Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu	260	265	270
Thr Trp Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln	275	280	285
Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg	290	295	300
Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu	305	310	315

Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	320	325	330
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	335	340	345
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	350	355	360
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	365	370	375
Glu	Asp	Phe	Arg	Leu	His	Phe	Arg	Asn	Ile	Ser	Arg	Ile	Met	Asp	380	385	390
Cys	Val	Gly	Cys	Phe	Lys	Cys	Arg	Leu	Trp	Gly	Lys	Leu	Gln	Thr	395	400	405
Gln	Gly	Leu	Gly	Thr	Ala	Leu	Lys	Ile	Leu	Phe	Ser	Glu	Lys	Leu	410	415	419
Ile	Ala	Asn	Met	Pro	Glu	Ser	Gly	Pro	Ser	Tyr	Glu	Phe	His	Leu	425	430	435
Thr	Arg	Gln	Glu	Ile	Val	Ser	Leu	Phe	Asn	Ala	Phe	Gly	Arg	Ile	440	445	450
Ser	Thr	Ser	Val	Lys	Glu	Leu	Glu	Asn	Phe	Arg	Asn	Leu	Leu	Gln	455	460	465
Asn Ile His																	

<210> 318

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 101, 263, 376, 397, 426

<223> unknown base

<400> 338

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ttaaaagacc tttaaattct ttggcttctg gtcaagggaac aagtgaagag 100
nacaattttt acagttgggt agaaggtctc tgtgtagaaa aaagagcatt 150
ctacagactt atatctgggc tacatgcaag cattaatgtg catttgagtg 200
caagatatct ttacaagag acctggttag aaaagaaatg gggacacaaac 250
attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300
tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350

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ctttatccaa agtggtacca ttcttngagc gccagattt tcaactnttt 400
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450
acttcatgaa atcaagtcac ttcccttgca ttttgatgag aattcatttt 500
tttactg 507

<210> 339

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 339

aaactccgg agctgcaatg 20

<210> 340

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 340

ttacttctta atcctgagcg c 21

<210> 341

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

aaaggaggac ttctgactgc 20

<210> 342

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

agagattcat ccactgctcc aagtcg 26

<210> 343

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

tgccagaaa cagcacata tcagc 25

<210> 344

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

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gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100

ggactttctc tactggacag aaaccgatca ggcattggaac tccccttcgt 150

cactcaacctg ttcttgcccc tgggtgttcct gacaggtctc tgcctccccct 200

ttaccctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250

gaatttgat acagtgtctt acaacatggt ggggggtggac agcgatggat 300

gctgggtggc gccccttggg atgggccttc aggcgacccg aggggggacg 350

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cacttaggtg actaccaact gggaaattca tctcatcttg ctgtgaatat 450

gcacctggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500

tgagctaagg agaggggtgt ggcagtgtct ctgaaggctc ataaaagaaa 550

aaagagaagt gtggtaaggg aaaatggtct gtgtggaggg gtcaaggagt 600

taaaaacct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650

gcctcttca actgggagca tgttttgagg gtgcctccc aagcctggga 700

gtactatct ccccatccc caggcctgtg cccctctctg gtctcgtgt 750

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 gcttggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
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 agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346

<211> 124

<212> PRT

<213> Homo sapiens

<400> 346

Met	Glu	Leu	Pro	Phe	Val	Thr	His	Leu	Phe	Leu	Pro	Leu	Val	Phe
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Leu	Thr	Gly	Leu	Cys	Ser	Pro	Phe	Asn	Leu	Asp	Glu	His	His	Pro
				20					25					30
Arg	Leu	Phe	Pro	Gly	Pro	Pro	Glu	Ala	Glu	Phe	Gly	Tyr	Ser	Val
				35					40					45
Leu	Gln	His	Val	Gly	Gly	Gly	Gln	Arg	Trp	Met	Leu	Val	Gly	Ala
				50					55					60
Pro	Trp	Asp	Gly	Pro	Ser	Gly	Asp	Arg	Arg	Gly	Asp	Val	Tyr	Arg
				65					70					75
Cys	Pro	Val	Gly	Gly	Ala	His	Asn	Ala	Pro	Cys	Ala	Lys	Gly	His
				80					85					90
Leu	Gly	Asp	Tyr	Gln	Leu	Gly	Asn	Ser	Ser	His	Pro	Ala	Val	Asn
				95					100					105
Met	His	Leu	Gly	Met	Ser	Leu	Leu	Glu	Thr	Asp	Gly	Asp	Gly	Gly
				110					115					120

Pho Met Val Ser

<210> 247

<211> 109

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 11

<223> unknown base

<400> 347

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ggatctgaac tccccttctg cactcacctg ttcttgcccc tgggtgttct 200
caataggtctc tgetccccc ttaacctgga tgaacatcac ccacgcctat 250
tcccaaggcc accagaagct gaatttggat acagtgtctt acaacatggt 300
gggggtggac agcgatggat gctgggtggg gccccctggg atgggccttc 350
aggagacagg aggggggaag ttatctgctg cctgttaggg ggggccaca 400
atgcccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
ctctcatctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500
tggtgatgg 509

<210> 348

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 348

agggacagag gccagaggac ttc 23

<210> 349

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 349

caagtgcata ttcacagcag gatg 24

<210> 350

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 350

ggaactcccc ttctgaactc acctgttctt gcccttggtg ttct 45

<210> 351

<211> 2056

<212> DNA

<213> Homo sapiens

<400> 351

aagttacat ttctcttgga actctcctag gccactcctt gctgatgcaa 50

ttcttggtt tgggcagaaa ggagggtgtt tggagcccg cctttctga 100

gttccctggg ccggtcttag aacattcag gcttctgtgc gactcagacc 150

ttagctccaa catatgcatt ctgaagaaag atggttgaga tggacagaat 200

gtttatctt ggaaagaaac aatgttctag gtcaaaactga gtctaccaa 250

ttagacttt cacaatggtt ctagaagaaa tctggacaag tcttttcctg 300

tggttttct acgcattgat tccatgtttg ctccacagatg aagtggccat 350

tctgcttgcc cctcagaacc tctctgtact ctcaaccacc atgaagcacc 400

tcttgatgtg gagccagtg atcgccctg gagaaacagt gtaattctt 450

gtcgaatacc agggggagta cgaagacctg tacaagagcc acatctggat 500

ccccagcagc tgggtgtcac tcaatgaagg tctgagtgt gatgtcactg 550

atgacatcac ggccactgtg ccatacaacc ttctgtgtcag ggccacattg 600

ggctcacaga cctcagcctg gagcatcctg aagcatcctt ttaatagaaa 650

ctcaaccacc cttaccagac ctgggatgga gatcaccaaa gatggcttcc 700

acctggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750

gctactgga ggaggagcc tgggtccagag gaacatgtca aaatggtgag 800

gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcct 850

actgtgtgaa ggccagaca ttctggaagg ccattgggag gtacagagcc 900

ttcagccaga cagaatgtgt ggaggtgcaa ggagaggcca ttcccttggt 950

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 aaaaaa 2056

4210 - 351

4211 - 311

4212 - PR7

4213 - Homo sapiens

4400 - 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
1					5					10				15

Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
					20				25					30

Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser	45	40	45
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro	50	55	60
Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu	65	70	75
Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser	80	85	90
Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala	95	100	105
Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln	110	115	120
Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser	125	130	135
Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe	140	145	150
His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe	155	160	165
Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val	170	175	180
Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met	185	190	195
Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys	200	205	210
Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu	215	220	225
Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe	230	235	240
Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp	245	250	255
Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val	260	265	270
Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile	275	280	285
Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met	290	295	300
Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser	305	310	

<210> 353
<211> 864
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 654, 711, 743, 827
<223> unknown base

<400> 353
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tacccttcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150
agaatgcttt attttgaaa gaaacaatgt tetaggtcaa actgagtcta 200
cccaatgcag accttcacaa tggttctaga agaaatctgg acaagtcttt 250
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accattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
gcctctcttg atgtggagcc cagtgtctgc gcttgagaa acagtgtact 400
attctgtcga ataccagggg gagtaagaga gctgtacac gagccacata 450
tggatcccca gcagctcgtg ctcaactcact gaaggctctg agtgtgatgt 500
cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcc 550
cattgggctc acagacctca gcttgagca tctgaagca tccctttaat 600
agaaactcaa ccatccttac ccgacctggg atggagatca ccaaagatgg 650
cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700
ttgtggccta ntggaggagg ggogaacccc ttgcggcgca aggggttngc 750
gaaccccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800
tgaccccat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850
ggcgctgggt tgat 864

<210> 354
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 354
agcttccgt gcgactagac ctc 23

<210> 355
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 355
ctgggtggg taaggatggt tgag 24

<210> 356
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 356
tttttaagca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA
<213> Homo sapiens

<400> 357
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agaggcagga gctggaaagg agagaggag gaggaggagg agatgcggga 200
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<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

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Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp
			20						25				30	

Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
			35					40				45		

Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
			50					55					60	

Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu	65	70	75
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser	80	85	90
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg	95	100	105
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser	110	115	120
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu	125	130	135
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn	140	145	150
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln	155	160	165
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly	170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn	185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile	200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu	215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser	230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile	245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg	260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser	275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg	290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro	305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg	320	325	

<210> 359

<211> 24

<210> DNA
<211> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 359
tctgttgagg tgcagctcat tcaa 24

<210> 260
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 260
aaagctcttg aagatctgag atgg 24

<210> 161
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 361
gactcttttgt caagcttgcc agtaactcta aaccattcct cagtcgcctc 50

<210> 362
<211> 3038
<212> DNA
<213> Homo sapiens

<400> 362
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<10> 363

<11> 500

<12> PET

<13> Homo sapiens

<400> 363

Met	Lys	Cys	Thr	Ala	Arg	Glu	Trp	Leu	Arg	Val	Thr	Thr	Val	Leu
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Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20					25					30

Leu Leu Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu	35	40	45
Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn	50	55	60
Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln	65	70	75
Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val	80	85	90
Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp	95	100	105
Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu	110	115	120
Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln	125	130	135
Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His	140	145	150
Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys	155	160	165
Thr His Tyr Thr Glu Val Val Trp Ala Thr Ser Asn Arg Ile Gly	170	175	180
Cys Ala Ile Asn Leu Cys His Asn Met Asn Ile Trp Gly Gln Ile	185	190	195
Trp Pro Lys Ala Val Tyr Leu Val Cys Asn Tyr Ser Pro Lys Gly	200	205	210
Asn Trp Trp Gly His Ala Pro Tyr Lys His Gly Arg Pro Cys Ser	215	220	225
Ala Cys Pro Pro Ser Phe Gly Gly Gly Cys Arg Glu Asn Leu Cys	230	235	240
Tyr Lys Glu Gly Ser Asp Arg Tyr Tyr Pro Pro Arg Glu Glu Glu	245	250	255
Thr Asn Glu Ile Glu Arg Gln Gln Ser Gln Val His Asp Thr His	260	265	270
Val Arg Thr Arg Ser Asp Asp Ser Ser Arg Asn Glu Val Ile Ser	275	280	285
Ala Gln Gln Met Ser Gln Ile Val Ser Cys Glu Val Arg Leu Arg	290	295	300
Asp Gln Cys Lys Gly Thr Thr Cys Asn Arg Tyr Glu Cys Pro Ala	305	310	315

Gly Cys Leu Asp Ser Lys Ala Lys Val Ile Gly Ser Val His Tyr	320	325	330
Glu Met Gln Ser Ser Ile Cys Arg Ala Ala Ile His Tyr Gly Ile	335	340	345
Ile Asp Asn Asp Gly Gly Trp Val Asp Ile Thr Arg Gln Gly Arg	350	355	360
Lys His Tyr Phe Ile Lys Ser Asn Arg Asn Gly Ile Gln Thr Ile	365	370	375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe Thr Val Ser Lys Val Thr	380	385	390
Val Glu Ala Val Thr Cys Glu Thr Thr Val Glu Gln Leu Cys Pro	395	400	405
Ile His Lys Pro Ala Ser His Cys Pro Arg Val Tyr Cys Pro Arg	410	415	420
Asn Cys Met Gln Ala Asn Pro His Tyr Ala Arg Val Ile Gly Thr	425	430	435
Arg Val Tyr Ser Asp Leu Ser Ser Ile Cys Arg Ala Ala Val His	440	445	450
Ala Gly Val Val Arg Asn His Gly Gly Tyr Val Asp Val Met Pro	455	460	465
Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile	470	475	480
Ile Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg	485	490	495
Val Phe Ala Val Val	500		

<110> 364

<111> 24

<112> RNA

<113> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

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<210> 365

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365

ccacagaggtat actgtectcg 20

<210> 366

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 366

attacagatt ttctctacag cccc 25

<210> 367

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 367

attactcca gcatgtactg ctgc 24

<210> 368

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 368

ccatttcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369

<211> 1685

<212> DNA

<213> Homo sapiens

<400> 369

gcacagacaaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50

ccacacgacgg cgcagccgga gccagcagag ccggaaggcg cgcgccgggc 100

agaaaaagcc gagcagagct gggcggcgtc tccgggcgcg cgcctcgcacg 150

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<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

Met	Ser	Leu	Leu	Pro	Arg	Arg	Ala	Pro	Pro	Val	Ser	Met	Arg	Leu
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Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala	
				20				25						30
Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys
				35				40						45
Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr
				50				55						60
Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val
				65				70						75
Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln
				80				85						90
Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys
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Arg	Arg	Val	Tyr	Glu	Glu									
				110										

<210> 371

<211> 22

<212> RNA

<213> Artificial Sequence

<300>

<223> Synthetic oligonucleotide probe

<400> 371

caagggccctc cccatgtacc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<300>

<223> Synthetic oligonucleotide probe

<400> 372

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<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<300>

<223> Synthetic oligonucleotide probe

<400> 373

ctccgggtcag catgaggetc ctggcgggcgg ctgctcctgc tgcgc 45

<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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caaaatccgg ggctaagaa cacggttacc caatgagatc ttgggtccag 200

tggagagta cttaggggtc cccatgctt cacccccac tggagagagg 250

agggttcagg cccagagacc ccgtctcttc tggactggca tccgaatatc 300

tactcagttc gctgctgtgt gcacccagca cctggatgag agatccttac 350

tgcctgacat gctgcacata tggtttacgg caaatttgga tactttgatg 400

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gcacacggga gatggagcca acacaaagaa aaacgcagat gatataacga 500

gtaatgacgg tgggtcaagac gaagatattc atgatcagaa cagtaagaag 550

ccgtcattgg totatatcca tgggggatct tacatggagg gcacccggca 600

catgattgac ggcagcattt tggcaagcta cggaaaagtc atcgtgatca 650

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cactactcag aaggtctctt ccagaaggcc atcattcaga ggggcacccc 900

cctgtccagc tgggcagtga actaccagcc ggccaagtac actcggatat 950

tggcagacaa ggtcggctgc aacatgctgg acaccaogga catggttagaa 1000

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 taagaactt tct 3113

>210: 375

>211: 816

>212: PRT

>213: Homo sapiens

>400: 375

Met	Leu	Asn	Ser	Asn	Val	Leu	Leu	Trp	Leu	Thr	Ala	Leu	Ala	Ile
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Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn
				20					25					30
Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
				35					40					45
Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala
				50					55					60
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro
				65					70					75
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val
				80					85					90
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu
				95					100					105
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val
				110					115					120
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro
				125					130					135
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr
				140					145					150

Ser Asn Asp Arg Gly Glu Asp Glu Asp Ile His Asp Gln Asn Ser	155	160	165
Lys Lys Pro Val Met Val Tyr Ile His Gly Gly Ser Tyr Met Glu	170	175	180
Gly Thr Gly Asn Met Ile Asp Gly Ser Ile Leu Ala Ser Tyr Gly	185	190	195
Asn Val Ile Val Ile Thr Ile Asn Tyr Arg Leu Gly Ile Leu Gly	200	205	210
Phe Leu Ser Thr Gly Asp Gln Ala Ala Lys Gly Asn Tyr Gly Leu	215	220	225
Leu Asp Gln Ile Gln Ala Leu Arg Trp Ile Glu Glu Asn Val Gly	230	235	240
Ala Phe Gly Gly Asp Pro Lys Arg Val Thr Ile Phe Gly Ser Gly	245	250	255
Ala Gly Ala Ser Lys Val Ser Leu Leu Thr Leu Ser His Tyr Ser	260	265	270
Glu Gly Leu Phe Gln Lys Ala Ile Ile Gln Ser Gly Thr Ala Leu	275	280	285
Ser Ser Trp Ala Val Asn Tyr Gln Pro Ala Lys Tyr Thr Arg Ile	290	295	300
Leu Ala Asp Lys Val Gly Cys Asn Met Leu Asp Thr Thr Asp Met	305	310	315
Val Glu Cys Leu Arg Asn Lys Asn Tyr Lys Glu Leu Ile Gln Gln	320	325	330
Thr Ile Thr Pro Ala Thr Tyr His Ile Ala Phe Gly Pro Val Ile	335	340	345
Asp Gly Asp Val Ile Pro Asp Asp Pro Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu Asn Tyr Asp Ile Met Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys Phe Val Asp Gly Ile Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn Asp Phe Asp Phe Ser Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly Tyr Pro Glu Gly Lys Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met Tyr Thr Asp Trp Ala Asp Lys Glu Asn Pro Glu	425	430	435

Thr Arg Arg Lys Thr Leu Val Ala Leu Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala Val Ala Ala Asp Leu His Ala Gln Tyr Gly Ser	455	460	465
Phe Thr Tyr Phe Tyr Ala Phe Tyr His His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp Ala Asp Ser Ala His Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile Pro Met Ile Gly Pro Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys Asn Asp Val Met Leu Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr Lys Phe Ile His Thr Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp Ser Lys Tyr Asn Pro Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu Lys Pro Arg Val Arg Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe Trp Leu Glu Leu Val Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe Gln Tyr Val Ser Thr Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr Ser Phe Pro Tyr Gly Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro Thr Thr Lys Arg Pro Ala Ile Thr Pro Ala Asn	635	640	645
Asn Pro Lys His Ser Lys Asp Pro His Lys Thr Gly Pro Glu Asp	650	655	660
Thr Thr Val Leu Ile Glu Thr Lys Arg Asp Tyr Ser Thr Glu Leu	665	670	675
Ser Val Thr Ile Ala Val Gly Ala Ser Leu Leu Phe Leu Asn Ile	680	685	690
Leu Ala Phe Ala Ala Leu Tyr Tyr Lys Lys Asp Lys Arg Arg His	695	700	705
Glu Thr His Arg Arg Pro Ser Pro Gln Arg Asn Thr Thr Asn Asp	710	715	720

Ile	Ala	His	Ile	Gln	Asn	Glu	Glu	Ile	Met	Ser	Leu	Gln	Met	Lys
									730					735
Gln	Leu	Glu	His	Asp	His	Glu	Cys	Glu	Ser	Leu	Gln	Ala	His	Asp
									745					750
Thr	Leu	Arg	Leu	Thr	Cys	Pro	Pro	Asp	Tyr	Thr	Leu	Thr	Leu	Arg
									760					765
Arg	Ser	Pro	Asp	Asp	Ile	Pro	Leu	Met	Thr	Pro	Asn	Thr	Ile	Thr
									775					780
Met	Ile	Pro	Asn	Thr	Leu	Thr	Gly	Met	Gln	Pro	Leu	His	Thr	Phe
									790					795
Asn	Thr	Phe	Ser	Gly	Gly	Gln	Asn	Ser	Thr	Asn	Leu	Pro	His	Gly
									805					810
His	Ser	Thr	Thr	Arg	Val									
									815					

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 <113> Artificial Sequence

<120>
 <123> Synthetic oligonucleotide probe

<400> 376
 ggcaagctac ggaaacgtca tegtg 25

<110> 377
 <111> 25
 <112> DNA
 <113> Artificial Sequence

<120>
 <123> Synthetic oligonucleotide probe

<400> 377
 aaccctccgag ccaaaagatg gtcac 25

<110> 378
 <111> 47
 <112> DNA
 <113> Artificial Sequence

<120>
 <123> Synthetic oligonucleotide probe

<400> 378
 gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<110> 379
 <111> 2461
 <112> DNA

<213> Homo sapiens

<400> 379

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cgagtacttg aaacgggagc actggtgtg gaagccctac cagggtgtgg 200
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 <211> 348
 <212> PRT
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<400> 380
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 20 25 30

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Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu Ser Lys Pro	50	55	60
Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu Met	65	70	75
Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp	80	85	90
Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe	95	100	105
Leu Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln	110	115	120
Gly Lys Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr	125	130	135
Lys Asp Arg Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys	140	145	150
Phe Val Gly Leu Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu	155	160	165
Lys Gln Gln Glu Arg Val Phe Pro Tyr Ile Ser Ala Met Val Asn	170	175	180
Asn Gly Ser Leu Ser Tyr Asp His Glu Arg Asp Gly Arg Pro Thr	185	190	195
Glu Leu Gly Gly Cys Thr Ala Ile Val Arg Asn Leu His Tyr Asp	200	205	210
Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile Met	215	220	225
Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val	230	235	240
Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser	245	250	255
Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys	260	265	270
Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu	275	280	285
His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro	290	295	300
Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe	305	310	315

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val
320 325 330

Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys
335 340 345

Arg Phe Tyr

<110> 351

<111> 27

<112> DNA

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<123> Synthetic oligonucleotide probe

<100> 381

cttgggttcg tggcagcagt gg 22

<110> 382

<111> 21

<112> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<100> 382

caatctctag gctgcatgct cagg 24

<110> 383

<111> 45

<112> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<100> 383

gtcacaacgtt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<110> 384

<111> 3150

<112> DNA

<113> Homo sapiens

<100> 384

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tgggggtctgg ctccagaattc ctgcagctgg tgaaaatctg ttttctagaa 200

gagggtttaat taatgactgc agtctgacat gttcccgatt tgagggtgaaa 250
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<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

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Pro Val Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys
35 40 45

Arg Ile Met Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro
50 55 60

Val Tyr Glu Ala Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu
65 70 75

Arg Ser Met Glu Gly His Ala Pro His His Phe Lys Leu Val Ser
80 85 90

Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro Leu Tyr Val
47 100 105

Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu Val Ala
110 115 120

Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser His
125 130 135

Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser
140 145 150

Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu
155 160 165

Thr Gln Thr Gly Val Val Gln His Leu Gln Asn Gly Gln Leu Leu
170 175 180

Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro Asn Asp Trp
185 190 195

Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg Thr
200 205 210

Leu Gln Ser Gly Leu Ala Leu Leu Tyr Gly Phe Leu Pro Asp Phe
115 220 325

Asp Trp Lys Lys Ile Tyr Phe Arg His Gln Pro Ser Ala Leu Phe
230 235 240

Cys Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu	245	250	255
Lys Gln Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln	260	265	270
Leu Glu Lys Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro	275	280	285
Thr Lys Gln Leu Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys	290	295	300
His Phe Cys His Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys	305	310	315
Val Asp Met Glu His Phe Lys Val Ile Lys Thr His Gln Ile Gln	320	325	330
Asp Glu Arg Glu Arg Arg Glu Lys Lys Leu Tyr Phe Gly Tyr Ser	335	340	345
Leu Leu Gly Ala His Pro Ile Leu Asn Gln Thr Ile Gly Arg Met	350	355	360
Gln Arg Ala Thr Glu Gly Arg Lys Glu Glu Leu Phe Ala Leu Tyr	365	370	375
Ser Ala His Asp Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly	380	385	390
Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe	395	400	405
Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg	410	415	420
Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr Ser Phe Cys	425	430	435
Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro Leu Glu	440	445	450
Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly	455	460	465
Gly Ser Gly Thr Asn Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe	470	475	480

010 386

011 24

012 DNA

013 Artificial Sequence

020

023 Synthetic oligonucleotide probe

<400> 386
cgaacagct tagagctcca gacc 24

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<10>
<13> Synthetic oligonucleotide probe

<400> 387
cttctatgc tetgtattgg catgg 25

<10> 388
<11> 50
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<13> Artificial Sequence

<10>
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gggacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

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<12> DNA
<13> Homo sapiens

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<310> 390
 <311> 316
 <312> PRT
 <313> Homo sapiens

<400> 390

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Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	

Asp Lys Ala Ala Gln Val Phe Lys Leu Asp Cys Asn Ser Gly Thr	290	295	300
Ile Ser Thr Ile Gly Glu Leu Asp His Glu Glu Ser Gly Phe Tyr	305	310	315
Gln Met Glu Val Gln Ala Met Asp Asn Ala Gly Tyr Ser Ala Arg	320	325	330
Ala Lys Val Leu Ile Thr Val Leu Asp Val Asn Asp Asn Ala Pro	335	340	345
Glu Val Val Leu Thr Ser Leu Ala Ser Ser Val Pro Glu Asn Ser	350	355	360
Pro Arg Gly Thr Ile Ile Ala Leu Leu Asn Val Asn Asp Gln Asp	365	370	375
Ser Glu Glu Asn Gly Gln Val Ile Cys Phe Ile Gln Gly Asn Leu	380	385	390
Pro Phe Lys Leu Glu Lys Ser Tyr Gly Asn Tyr Tyr Ser Leu Val	395	400	405
Thr Asp Ile Val Leu Asp Arg Glu Gln Val Pro Ser Tyr Asn Ile	410	415	420
Thr Val Thr Ala Thr Asp Arg Gly Thr Pro Pro Leu Ser Thr Glu	425	430	435
Thr His Ile Ser Leu Asn Val Ala Asp Thr Asn Asp Asn Pro Pro	440	445	450
Val Phe Pro Gln Ala Ser Tyr Ser Ala Tyr Ile Pro Glu Asn Asn	455	460	465
Pro Arg Gly Val Ser Leu Val Ser Val Thr Ala His Asp Pro Asp	470	475	480
Cys Glu Glu Asn Ala Gln Ile Thr Tyr Ser Leu Ala Glu Asn Thr	485	490	495
Ile Gln Gly Ala Ser Leu Ser Ser Tyr Val Ser Ile Asn Ser Asp	500	505	510
Thr Gly Val Leu Tyr Ala Leu Ser Ser Phe Asp Tyr Glu Gln Phe	515	520	525
Arg Asp Leu Gln Val Lys Val Met Ala Arg Asp Asn Gly His Pro	530	535	540
Pro Leu Ser Ser Asn Val Ser Leu Ser Leu Phe Val Leu Asp Gln	545	550	555
Asn Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp	560	565	570

Gly Ser Thr Gly	Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly	575	580	585
Tyr Leu Val Thr	Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln	590	595	600
Asn Ala Trp Leu	Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly	605	610	615
Leu Phe Ser Val	Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg	620	625	630
Ala Leu Leu Asp	Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala	635	640	645
Val Gln Asp His	Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu	650	655	660
Thr Val Ala Val	Asp Asp Ser Ile Pro Gln Val Leu Ala Asp Leu	665	670	675
Gly Ser Leu Glu	Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr	680	685	690
Leu Tyr Leu Val	Val Ala Val Ala Ala Val Ser Cys Val Phe Leu	695	700	705
Ala Phe Val Ile	Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His	710	715	720
Lys Ser Arg Leu	Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala	725	730	735
Pro Ala Ser His	Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu	740	745	750
Gln Thr Tyr Ser	His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys	755	760	765
Ser His Leu Ile	Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val	770	775	780
Ser Gln Glu Ser	Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly	785	790	795
Asp Ser Val Phe	Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser	800	805	810
Leu Tyr Gln Ile	Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser	815	820	825
Gln Ala Gly Val	Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln	830	835	840
Thr Pro Arg Leu	Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn	845	850	855

Arg Asp Tyr Arg Cys Lys Pro Pro Thr Val Cys Leu Ser Ile Tyr
 860 865 870

Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Leu Leu
 875 880 885

Pro Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp
 890 895 900

Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro
 905 910 915

<114>

<116> 391

<117> 23

<118> DNA

<119> Artificial Sequence

<120>

<121> Synthetic oligonucleotide probe

<130> 391

<131> tcaatctctg tgaaccgccc cac 23

<140> 392

<141> 24

<142> DNA

<143> Artificial Sequence

<150>

<151> Synthetic oligonucleotide probe

<160> 392

<161> ctctggggcca ttgtcgttct ggtc 24

<170> 393

<171> 40

<172> DNA

<173> Artificial Sequence

<180>

<181> Synthetic oligonucleotide probe

<190> 393

<191> ccgactgtga aagagaacgc cccagatcca ctgtgtcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

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<402> cccagttaaa aggtccaga atcgtgtacc aggcagagaa ctgaagtact 100

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(210) 395

(211) 260

(212) PET

(213) Homo sapiens

(400) 395

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			20						25					30

Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45

Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60

Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75

Leu	His	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn
					80				85					90
Leu	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro
					95				100					105
His	Pro	Cys	Tyr	Am	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp
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Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys
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Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln
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Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Gln
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Am	His	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Gln	Val	Lys	Ile	Phe	Pro
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Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly
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Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly
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Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly
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Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 396

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<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

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<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<223>

<223> Synthetic oligonucleotide probe

<400> 398

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<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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ggaaccgggc ggattcccg gcgctcaaac caccgatcc cataaaacat 250
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cccagccaga gccggggcga ggggagcgcg ccgagcctcg tccgcgcgc 400
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<210> 400

<211> 473

<212> PRT
<213> Homo sapiens

<400> 400

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			20						25					30
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln
				35					40					45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln
				50					55					60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala
				65					70					75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser
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Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala
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Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser
				110					115					120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu
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His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe
				140					145					150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala
				155					160					165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu
				170					175					180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu
				185					190					195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His
				200					205					210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu
				215					220					225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala
				230					235					240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu
				245					250					255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro
				260					265					270

Leu Trp Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val	275	280	285
Pro Cys Ser Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg	290	295	300
Leu Ala Ala Asn Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro	305	310	315
Tyr His Pro Ile Trp Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu	320	325	330
Gly Leu Pro Lys Cys Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser	335	340	345
Val Leu Glu Pro Gly Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys	350	355	360
Gly Arg Val Pro Pro Gly Asp Ser Pro Pro Gly Asn Gly Ser Gly	365	370	375
Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly Ser	380	385	390
Ala Glu Pro Pro Leu Thr Ala Val Arg Pro Glu Gly Ser Glu Pro	395	400	405
Pro Gly Phe Pro Thr Ser Gly Pro Arg Arg Arg Pro Gly Cys Ser	410	415	420
Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly	425	430	435
Ser Gly Gly Gly Gly Thr Gly Asp Ser Glu Gly Ser Gly Ala Leu	440	445	450
Pro Ser Leu Thr Cys Ser Leu Thr Pro Leu Gly Leu Ala Leu Val	455	460	465
Leu Trp Thr Val Leu Gly Pro Cys	470		

<E10> 401

<E11> 24

<E12> DNA

<E13> Artificial Sequence

<E20>

<E25> Synthetic oligonucleotide probe

<E30> 401

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<E10> 402

<E11> 24

<E12> DNA

<213> Artificial Sequence

<225>

<225> Synthetic oligonucleotide probe

<100> 402

actgcaggt cattggcagc tagg 24

<110> 403

<111> 45

<112> DNA

<113> Artificial Sequence

<127>

<127> Synthetic oligonucleotide probe

<100> 403

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<110> 404

<111> 2733

<112> DNA

<113> Homo sapiens

<100> 404

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<210> 405
 <211> 798
 <212> PRT
 <213> Homo sapiens

<400> 405
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 20 25 30
 Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe
 35 40 45
 Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe
 50 55 60
 Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His
 65 70 75
 Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys
 80 85 90
 Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu
 95 100 105
 Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala
 110 115 120
 Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu
 125 130 135
 Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly
 140 145 150

Thr Thr Phe Pro	Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln	155	160	165
Asn Asn Ile Glu	Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg	170	175	180
Val Leu Thr Arg	Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu	185	190	195
Val Leu Asp Lys	Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg	200	205	210
Leu Thr Leu Thr	Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly	215	220	225
Thr Ala Gln Val	Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala	230	235	240
Pro Glu Phe Glu	Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp	245	250	255
Ser Pro Val Gly	Phe Leu Val Val Lys Val Ser Ala Thr Asp Val	260	265	270
Asp Thr Gly Val	Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala	275	280	285
Ser Glu Glu Ile	Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly	290	295	300
Glu Ile Glu Leu	Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser	305	310	315
Tyr Glu Val Asn	Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly	320	325	330
Lys Cys Thr Val	Leu Ile Gln Val Ile Asp Val Asn Asp His Ala	335	340	345
Pro Glu Val Thr	Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn	350	355	360
Ala Pro Glu Thr	Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp	365	370	375
Ser Gly Glu Asn	Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu	380	385	390
Pro Phe Leu Leu	Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr	395	400	405
Glu Arg Pro Leu	Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr	410	415	420
Ile Thr Val Thr	Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu	425	430	435

Asn Met Thr Val	Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro	Ala
440	445	450	
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn	Ser
455	460	465	
Pro Ala Leu His	Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp	Ser
470	475	480	
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln	Asp
485	490	495	
Pro His Leu Pro	Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp	Asn
500	505	510	
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu	Gln
515	520	525	
Gly Phe Gln Phe	Arg Val Gly Ala Ser	Asp His Gly Ser Pro	Ala
530	535	540	
Leu Ser Ser Glu	Ala Leu Val Arg Val	Val Val Leu Asp Ala	Asn
545	550	555	
Asp Asn Ser Pro	Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser	Ala
560	565	570	
Pro Cys Thr Glu	Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr	Leu
575	580	585	
Val Thr Lys Val	Val Ala Val Asp Gly	Asp Ser Gly Gln Asn	Ala
590	595	600	
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu	Phe
605	610	615	
Gly Val Trp Ala	His Asn Gly Glu Val	Arg Thr Ala Arg Leu	Leu
620	625	630	
Ser Glu Arg Asp	Ala Ala Lys His Arg	Leu Val Val Leu Val	Lys
635	640	645	
Asp Asn Gly Glu	Pro Pro Arg Ser Ala	Thr Ala Thr Leu His	Val
650	655	660	
Leu Leu Val Asp	Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro	Glu
665	670	675	
Ala Ala Pro Thr	Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr	Leu
680	685	690	
Val Val Ala Leu	Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser	Val
695	700	705	
Leu Leu Phe Val	Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala	Ala
710	715	720	

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe
785 790 795

Asn Ile Gln

<210> 486

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 486

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<210> 407

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

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<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

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<400> 408

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<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

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 tgetgtgggt gctgggaact cccgtccggc gggtggaggt tccagaggaa 200
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<211> 360
 <212> FRT
 <213> Homo sapiens

<400> 410

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Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu
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Glu	Gln	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala
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Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Gln
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Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu
			140						145					150
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn
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Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg
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Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met
			185						190					195
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys
			200						205					210
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser
			215						220					225
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu
			230						235					240
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr
			245						250					255
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly

260	265	270
Ala Lys Pro Met	Ala Arg Phe Asn His	Thr Asp Arg Thr Leu Glu
275	280	285
Thr Leu Lys Ile	Phe Ile Phe Asn Gln	Thr Gly Ile Glu Ala Lys
290	295	300
Lys Asn Val Val	Val Thr Gln Ala Asp	Gln Ile Gly Pro Leu Pro
305	310	315
Ser Thr Leu Ile	Lys Ser Val Asp Trp	Leu Leu Val Phe Ser Leu
320	325	330
Phe Phe Leu Ile	Ser Phe Ile Met Tyr	Ala Thr Ile Arg Thr Glu
335	340	345
Ser Ile Arg Trp	Leu Ile Pro Gly Gln	Glu Gln Glu His Val Glu
350	355	360

<210> 411

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

atagagajcca gaagtggcgg aatc 24

<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttgt cctgg 25

<210> 413

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

aggtagtgac tgtactctag tctgtttta caccocgtgg tgccg 45

<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414
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 ggcctgggcg cgggctctt cctcttggc cagcccgact tctcctacaa 150
 cccagcaat tgcagccca tcccgatcaa cctgcagctg tgcacggca 200
 tcgaatacca gaacatggg ctgcaccaac tctggggcca cgaacccatg 250
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 gaattttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415
 <211> 295
 <212> PRT
 <213> Homo sapiens

<400> 415
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His Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln	20	25	30
Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val	35	40	45
Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu	50	55	60
Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln	65	70	75
Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp	80	85	90
Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp	95	100	105
Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln	110	115	120
Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro	125	130	135
Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro Gln Asp Asn Asp	140	145	150
Leu Cys Ile Pro Leu Ala Ser Ser Asp His Leu Leu Pro Ala Thr	155	160	165
Glu Glu Ala Pro Lys Val Cys Glu Ala Lys Lys Asn Lys Asn Asp	170	175	180
Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn Asp Phe Ala	185	190	195
Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg Asp Thr	200	205	210
Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu Asn	215	220	225
Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys	230	235	240
Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala	245	250	255
Pro Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile	260	265	270
Thr Ser Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg	275	280	285
Ile Ser Arg Ser Ile Arg Lys Leu Gln Cys			

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 416
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<210> 417
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 417
 ccttcacaggt gcaatgcaag ctgtc 25

<210> 418
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 418
 ctcttctctct ttggccagcc cgaattctcc tacaagcgca gaattgc 47

<210> 419
 <211> 1830
 <212> DNA
 <213> Homo sapiens

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 cgtgggtgt tctgtctgc gacagcctg ctcaactgct ccaacgccac 150
 gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200
 tctgtccat ggagcagatc aactggctgt cactggctct cctcgtggta 250
 tccaccccat ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300
 ccgtcggggc accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350
 tacgcattgt gccctgcatt gttgttggga cccaaaaccc atttgccttc 400

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cggccaaat gctcgccacc atgtccaacc ctctggcggt ccttgtggc 550
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aacatctgt ccactgcgg gggggggga aagggtcct tggggctcc 1800
gggagcaat tacaagcgc cactgaaa 1830

4114 420
 4115 560
 4116 PRT
 4118 Homo sapiens

4400 420
 Met Ala Gly Pro Thr Glu Ala Glu Thr Gly Leu Ala Glu Pro Arg
 1 5 10 15
 Ala Leu Cys Ala Gln Arg Gly His Arg Thr Tyr Ala Arg Arg Trp
 20 25 30
 Val Phe Leu Leu Ala Ile Ser Leu Leu Asn Cys Ser Asn Ala Thr
 35 40 45
 Leu Trp Leu Ser Phe Ala Pro Val Ala Asp Val Ile Ala Glu Asp
 50 55 60
 Leu Val Leu Ser Met Glu Gln Ile Asn Trp Leu Ser Leu Val Tyr
 65 70 75
 Leu Val Val Ser Thr Pro Phe Gly Val Ala Ala Ile Trp Ile Leu
 80 85 90
 Asp Ser Val Gly Leu Arg Ala Ala Thr Ile Leu Gly Ala Trp Leu
 95 100 105
 Asn Phe Ala Gly Ser Val Leu Arg Met Val Pro Cys Met Val Val
 110 115 120
 Gly Thr Gln Asn Pro Phe Ala Phe Leu Met Gly Gly Gln Ser Leu
 125 130 135
 Cys Ala Leu Ala Gln Ser Leu Val Ile Phe Ser Pro Ala Lys Leu
 140 145 150
 Ala Ala Leu Trp Phe Pro Glu His Gln Arg Ala Thr Ala Asn Met
 155 160 165
 Leu Ala Thr Met Ser Asn Pro Leu Gly Val Leu Val Ala Asn Val
 170 175 180
 Leu Ser Pro Val Leu Val Lys Lys Gly Glu Asp Ile Pro Leu Met
 185 190 195
 Leu Gly Val Tyr Thr Ile Pro Ala Gly Val Val Cys Leu Leu Ser
 200 205 210
 Thr Ile Cys Leu Trp Glu Ser Val Pro Pro Thr Pro Pro Ser Ala
 215 220 225
 Gly Ala Ala Ser Ser Thr Ser Glu Lys Phe Leu Asp Gly Leu Lys
 230 235 240
 Leu Gln Leu Met Trp Asn Lys Ala Tyr Val Ile Leu Ala Val Cys
 245 250 255

Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala	Leu Leu
260	265		270
Gln Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser	Gly
275	280		285
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly Ala	Leu
290	295		300
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu	Ala
305	310		315
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro	Phe
320	325		330
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala	Ala
335	340		345
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro	Val
350	355		360
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu	Gly
365	370		375
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly	Ile
380	385		390
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser	Glu
395	400		405
Pro Ser Leu Ser	Thr Cys Gln Gln Gly	Glu Asp Pro Leu Asp	Trp
410	415		420
Thr Val Ser Leu	Leu Leu Met Ala Gly	Leu Cys Thr Phe Phe	Ser
425	430		435
Cys Ile Leu Ala	Val Phe Phe His Thr	Pro Tyr Arg Arg Leu	Gln
440	445		450
Ala Glu Ser Gly	Glu Pro Pro Ser Thr	Arg Asn Ala Val Gly	Gly
455	460		465
Ala Asp Ser Gly	Pro Gly Val Asp Arg	Gly Gly Ala Gly Arg	Ala
470	475		480
Gly Val Leu Gly	Pro Ser Thr Ala Thr	Pro Glu Cys Thr Ala	Arg
485	490		495
Gly Ala Ser Leu	Glu Asp Pro Arg Gly	Pro Gly Ser Pro His	Pro
500	505		510
Ala Cys His Arg	Ala Thr Pro Arg Ala	Gln Gly Pro Ala Ala	Thr
515	520		525
Asp Ala Pro Ser	Arg Pro Gly Arg Leu	Ala Gly Arg Val Gln	Ala
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Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser
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Pro Trp Val Ile Thr
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<210> 421

<211> 24

<212> DNA

<213> Artificial Sequence

<20>

<223> Synthetic oligonucleotide probe

<100> 421

agtttctcag cctctctgga gcag 24

<210> 422

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<100> 422

gggttcata aacctggagc cttgg 25

<210> 423

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<100> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

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ccatcat'ttg ctgaagtggg ccaactagtt cccagtagg gggctctccc 100

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tggcct'gac ttggggctct gcttggttca taatcatcta actatgggac 200

aagggt'tgtc cggcagctct gggggaagga gcacggggct gatcaagcca 250

tccaggaaac actggaggac ttgtccagcc ttgaaagaac totagtgggt 300

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 aaaaaaaaaa aaa 4313

<210> 425
 <211> 1184
 <212> PFT
 <213> Homo sapiens

<400> 425
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Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val	35	40	45
Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg	50	55	60
Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu	65	70	75
Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg	80	85	90
Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu	95	100	105
Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His	110	115	119
Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe	125	130	135
Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu	140	145	150
Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly	155	160	165
Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe	170	175	180
Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu	185	190	195
Leu Ile Val Val Lys Glu Leu Asp Arg Glu Ile His Ser Phe Phe	200	205	210
Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser	215	220	225
Gly Thr Ser Leu Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn	230	235	240
Ser Pro Ala Phe Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu	245	250	255
Asp Ala Ala Pro Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp	260	265	270
Pro Asp Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys	275	280	285
His Met Pro Pro Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys	290	295	300

Thr	Gly	Gln	Val	Ile	Leu	Arg	Arg	Pro	Leu	Asp	Tyr	Glu	Lys	Asn	
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Pro	Ala	Tyr	Glu	Val	Asp	Val	Gln	Ala	Arg	Asp	Leu	Gly	Pro	Asn	
				320					325					330	
Pro	Ile	Pro	Ala	His	Cys	Lys	Val	Leu	Ile	Lys	Val	Leu	Asp	Val	
				335					340					345	
Asn	Asp	Asn	Ile	Pro	Ser	Ile	His	Val	Thr	Trp	Ala	Ser	Gln	Pro	
				350					355					360	
Ser	Leu	Val	Ser	Glu	Ala	Leu	Pro	Lys	Asp	Ser	Phe	Ile	Ala	Leu	
				365					370					375	
Val	Met	Ala	Asp	Asp	Leu	Asp	Ser	Gly	His	Asn	Gly	Leu	Val	His	
				380					385					390	
Cys	Trp	Leu	Ser	His	Glu	Leu	Gly	His	Phe	Arg	Leu	Lys	Arg	Thr	
				395					400					405	
Asn	Gly	Asn	Thr	Tyr	Met	Leu	Leu	Thr	Asn	Ala	Thr	Leu	Asp	Arg	
				410					415					420	
Glu	Gln	Trp	Pro	Lys	Tyr	Thr	Leu	Thr	Leu	Leu	Ala	Gln	Asp	Gln	
				425					430					435	
Gly	Leu	Gln	Pro	Leu	Ser	Ala	Lys	Lys	Gln	Leu	Ser	Ile	Gln	Ile	
				440					445					450	
Ser	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Val	Phe	Glu	Lys	Ser	Arg	Tyr	
				455					460					465	
Glu	Val	Ser	Thr	Arg	Glu	Asn	Asn	Leu	Pro	Ser	Leu	His	Leu	Ile	
				470					475					480	
Thr	Ile	Lys	Ala	His	Asp	Ala	Asp	Leu	Gly	Ile	Asn	Gly	Lys	Val	
				485					490					495	
Ser	Tyr	Arg	Ile	Gln	Asp	Ser	Pro	Val	Ala	His	Leu	Val	Ala	Ile	
				500					505					510	
Asp	Ser	Asn	Thr	Gly	Glu	Val	Thr	Ala	Gln	Arg	Ser	Leu	Asn	Tyr	
				515					520					525	
Glu	Glu	Met	Ala	Gly	Phe	Glu	Phe	Gln	Val	Ile	Ala	Glu	Asp	Ser	
				530					535					540	
Gly	Gln	Pro	Met	Leu	Ala	Ser	Ser	Val	Ser	Val	Trp	Val	Ser	Leu	
				545					550					555	
Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	Glu	Val	Val	Gln	Pro	Val	Leu	
				560					565					570	
Ser	Asp	Gly	Lys	Ala	Ser	Leu	Ser	Val	Leu	Val	Asn	Ala	Ser	Thr	
				575					580					585	

Gly His Leu Leu Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly Pro
590	595 600
Ala Gly Thr Asp Thr Pro Pro Leu Ala Thr His Ser Ser Arg Pro	
605	610 615
Phe Leu Leu Thr Thr Ile Val Ala Arg Asp Ala Asp Ser Gly Ala	
620	625 630
Asn Gly Glu Pro Leu Tyr Ser Ile Arg Asn Gly Asn Glu Ala His	
635	640 645
Leu Phe Ile Leu Asn Pro His Thr Gly Gln Leu Phe Val Asn Val	
650	655 660
Thr Asn Ala Ser Ser Leu Ile Gly Ser Glu Trp Glu Leu Glu Ile	
665	670 675
Val Val Glu Asp Gln Gly Ser Pro Pro Leu Gln Thr Arg Ala Leu	
680	685 690
Leu Arg Val Met Phe Val Thr Ser Val Asp His Leu Arg Asp Ser	
695	700 705
Ala Arg Lys Pro Gly Ala Leu Ser Met Ser Met Leu Thr Val Ile	
710	715 720
Cys Leu Ala Val Leu Leu Gly Ile Phe Gly Leu Ile Leu Ala Leu	
725	730 735
Phe Met Ser Ile Cys Arg Thr Glu Lys Lys Asp Asn Arg Ala Tyr	
740	745 750
Asn Cys Arg Glu Ala Glu Ser Thr Tyr Arg Gln Gln Pro Lys Arg	
755	760 765
Pro Gln Lys His Ile Gln Lys Ala Asp Ile His Leu Val Pro Val	
770	775 780
Leu Arg Gly Gln Ala Gly Glu Pro Cys Glu Val Gly Gln Ser His	
785	790 795
Lys Asp Val Asp Lys Glu Ala Met Met Glu Ala Gly Trp Asp Pro	
800	805 810
Cys Leu Gln Ala Pro Phe His Leu Thr Pro Thr Leu Tyr Arg Thr	
815	820 825
Leu Arg Asn Gln Gly Asn Gln Gly Ala Pro Ala Glu Ser Arg Glu	
830	835 840
Val Leu Gln Asp Thr Val Asn Leu Leu Phe Asn His Pro Arg Gln	
845	850 855
Arg Asn Ala Ser Arg Glu Asn Leu Asn Leu Pro Glu Pro Gln Pro	
860	865 870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Gln	935	940	945
Arg Asn Pro Val Gln Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala	1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Arg Cys Leu
1175 1180

<210> 436
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 437
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 437
gtgacgaga tgcttgggat gttg 24

<210> 438
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 438
tggacacctt cagtattgat gccaagacag gccaggteat tctgcgtoga 50

<210> 439
<211> 2937
<212> DNA
<213> Homo sapiens

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cctgggagaa ggcagaccgt gtgagggggg ctgtggcccc agcgtgctgt 100
ggcctcgggg agtgggaagt ggaggcagga gccttcccta cacttcgcca 150
tcagtttctt catcgactcc agcatcatga ttacctccca gatactattt 200
tttgatttg ggtggctttt ctcatgcgc caattgttta aagactatga 250
gatacgtcag tatgttgtac aggtgatctt ctccgtgacg ttgtcatttt 300

cttgcaccat gtttgagctc atcatctttg aaatcttagg agtattgaat 350
agcagctccc gttattttca ctgaaaatg aacctgtatg taattctgct 400
atctctggtt ttcctgggtg ctttttaaat tggctattct atttgagaca 450
atatacgaat actgcataaa caacgaatgc tttttctctg tctcttatgg 500
ctgaacttta tgtattttct ctggaaacta ggagatcctt ttcctattct 550
cagcccaaaa catgggatct tctcataga acagctcctc agccgggttg 600
gtgtgattgg agtgactctc atggctcttc tttctggatt tggtaetgct 650
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ggggaagtgc ataacaacac atcaggtttc tggggaatga taagaaagt 850
taacacttca gcatcaggaa gtgaaaatct tactcttatt caacagggaag 900
tggatgcttt ggaagaatta agcaggcagc ttttctgga aacagctgat 950
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ttttcatgga taacatcaat attgtttttg atcaggttgg gaaaacggat 1100
ctgtcacaaa gaggcattga gatcaactgt aattatctgg gaatccaatt 1150
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agcaaatggc accttgaact taagcctact acagactgtt agaggccagt 1550
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cattttataa acaacaaaaa tgcattggta gcatttttca ctttcatagc 1650
atactcttc ccgctcaggt gatactatga ccatgagtag catcagccag 1700

aacatgagag ggagaactaa ctcaagacaa tactcagcag agagcatccc 1750
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 gtgaaaaata cactggaact ctggggcaag acatgttat ggtagctgag 1850
 ccaaacacgt aggatctccg ttttaagggt cacatggaaa aggttatagc 1900
 ttgtccttga gattgactca ttaaaatcag agactgtaac aaaaaaaaaa 1950
 aaaaaaaaaa agggcgcccg cgactctaga gtcjacctgc agaagcttgg 2000
 ccgccatggc ccaacttggt tattgcagct tataatg 2037

<110> 430
 <111> 455
 <112> PRT
 <113> Homo sapiens

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 Leu Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe
 20 25 30
 Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser
 35 40 45
 Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe
 50 55 60
 Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp
 65 70 75
 Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val
 80 85 90
 Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu
 95 100 105
 His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe
 110 115 120
 Met Tyr Phe Phe Trp Lys Leu Gly Asp Pro Phe Pro Ile Leu Ser
 125 130 135
 Pro Lys His Gly Ile Leu Ser Ile Glu Gln Leu Ile Ser Arg Val
 140 145 150
 Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu Ser Gly Phe Gly
 155 160 165
 Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe Leu Arg Asn
 170 175 180
 Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu Leu Gln

	185	190	195
Thr Met Asp Met	Ile Ile Ser Lys Lys	Lys Arg Met Ala Met	Ala
	200	205	210
Arg Arg Thr Met	Phe Gln Lys Gly Glu	Val His Asn Lys Pro	Ser
	215	220	225
Gly Phe Trp Gly	Met Ile Lys Ser Val	Thr Thr Ser Ala Ser	Gly
	230	235	240
Ser Glu Asn Leu	Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu	Glu
	245	250	255
Glu Leu Ser Arg	Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr	Ala
	260	265	270
Thr Lys Glu Arg	Ile Glu Tyr Ser Lys	Thr Phe Lys Gly Lys	Tyr
	275	280	285
Phe Asn Phe Leu	Gly Tyr Phe Phe Ser	Ile Tyr Cys Val Trp	Lys
	290	295	300
Ile Phe Met Ala	Thr Ile Asn Ile Val	Phe Asp Arg Val Gly	Lys
	305	310	315
Thr Asp Pro Val	Thr Arg Gly Ile Glu	Ile Thr Val Asn Tyr	Leu
	320	325	330
Gly Ile Gln Phe	Asp Val Lys Phe Trp	Ser Gln His Ile Ser	Phe
	335	340	345
Ile Leu Val Gly	Ile Ile Ile Val Thr	Ser Ile Arg Gly Leu	Leu
	350	355	360
Ile Thr Leu Thr	Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys	Ser
	365	370	375
Ser Asn Val Ile	Val Leu Leu Leu Ala	Gln Ile Met Gly Met	Tyr
	380	385	390
Phe Val Ser Ser	Val Leu Leu Ile Arg	Met Ser Met Pro Leu	Glu
	395	400	405
Tyr Arg Thr Ile	Ile Thr Glu Val Leu	Gly Glu Leu Gln Phe	Asn
	410	415	420
Phe Tyr His Arg	Trp Phe Asp Val Ile	Phe Leu Val Ser Ala	Leu
	425	430	435
Ser Ser Ile Leu	Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro	Glu
	440	445	450
Lys Gln Met Ala	Pro		
	455		

<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 81, 113, 157, 224, 297
<223> unknown base

<400> 431
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tcgactcag caccatgatt acctccnga naactatttt tggatttggg 100
tggttttctc tencgcgcaa tgtttaaaga ctatgagata cgtcagtatg 150
ttgtaenigt gatctttctc gtgacgtttg ccattttctg caccatgttt 200
tggctcatca tttttgaaat cttnnggagta ttgaatagca gctcccgta 250
tttccactgg aaaatgaacc tgtgtgtaat tetgtgata ctggttttca 300
tggtgccctt ttacattggc tattttattg tgagcaatat ccgactactg 350
cataaacaac gactgctttt ttctgtctc ttatggetga cttttatgta 400
tttccag 407

<210> 432
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
<223> unknown base

<400> 432
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tattttttgg attcggggta gnttttttct atgcgccaat tgtttaaaga 150
ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgtttg 200
cattttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250
ttgaatagca gctcccgta tttccactgg aaaatgaacc tgtgtgtaat 300
tetgtgata ctggttttca tggtgccctt ttacattggc tattttattg 350
tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400
ttatggetga cttttatgta tttntnttgg aaantaggag atccctttcc 450

<210> 457

<211> 20

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 433

atgagagcc ggagccttc 20

<210> 434

<211> 22

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 434

tccttcttta tgcagtagtc gg 22

<210> 435

<211> 41

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 435

attgtttaaa gactatgaga tacgtcagta tgttgtacag g 41

<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 436

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gggcctccgg gatttgcac ctttttggt cctgctcgt cgaactgctc 100

ttctcagggg ctgtgcctt caatctggac gtgatgggtg ccttgcccaa 150

ggagggcgag ccaggcagcc tcttcggctt ctctgtggcc ctgcacgggc 200

agttgcagcc ccgacccag agctggctgc tggtaggtgc tcccagggc 250

ctggctcttc ctgggcagca ggagaatgc actggaggcc tcttcgcttg 300

caggttgagc ctggaggaga ctgactgcta cagagtggac atcgaccagg 350

gagctgatat gcaaaaggaa agcaaggaga accagtgggtt gggagtcagt 400

gtttaggagcc agggggcctgg gggcaagatt gttacctgtg cacaccgata 450
tgaaggaaagg cagcagagtgg accagatcct ggagacgggg gatatgattg 500
ctccctgctt tgtgtctcagc caggacctgg ccattccggga tgagttaggat 550
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 a 3951

<110> 437
 <111> 1141
 <12> PRT
 <13> Homo sapiens

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 Cys Tyr Leu Phe Gly Ser Leu Leu Val Glu Leu Leu Phe Ser Arg
 20 25 30
 Ala Val Ala Phe Asn Leu Asp Val Met Gly Ala Leu Arg Lys Glu
 35 40 45
 Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg
 50 55 60
 Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro
 65 70 75
 Gln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly
 80 85 90
 Leu Phe Ala Cys Pro Leu Ser Leu Glu Glu Thr Asp Cys Tyr Arg
 95 100 105

Val Asp Ile Asp	Gln Gly Ala Asp Met	Gln Lys Glu Ser Lys Glu
110	115	120
Asn Gln Trp Leu	Gly Val Ser Val Arg Ser Gln Gly Pro Gly Gly	
125	130	135
Lys Ile Val Thr	Cys Ala His Arg Tyr Glu Ala Arg Gln Arg Val	
140	145	150
Asp Gln Ile Leu	Glu Thr Arg Asp Met Ile Gly Arg Cys Phe Val	
155	160	165
Leu Ser Gln Asp	Leu Ala Ile Arg Asp Glu Leu Asp Gly Gly Glu	
170	175	180
Trp Lys Phe Cys	Glu Gly Arg Pro Gln Gly His Glu Gln Phe Gly	
185	190	195
Phe Cys Gln Gln	Gly Thr Ala Ala Ala Phe Ser Pro Asp Ser His	
200	205	210
Tyr Leu Leu Phe	Gly Ala Pro Gly Thr Tyr Asn Trp Lys Gly Thr	
215	220	225
Ala Arg Val Glu	Leu Cys Ala Gln Gly Ser Ala Asp Leu Ala His	
230	235	240
Leu Asp Asp Gly	Pro Tyr Glu Ala Gly Gly Glu Lys Glu Gln Asp	
245	250	255
Pro Arg Leu Ile	Pro Val Pro Ala Asn Ser Tyr Phe Gly Phe Ser	
260	265	270
Ile Asp Ser Gly	Lys Gly Leu Val Arg Ala Glu Glu Leu Ser Phe	
275	280	285
Val Ala Gly Ala	Pro Arg Ala Asn His Lys Gly Ala Val Val Ile	
290	295	300
Leu Arg Lys Asp	Ser Ala Ser Arg Leu Val Pro Glu Val Met Leu	
305	310	315
Ser Gly Glu Arg	Leu Thr Ser Gly Phe Gly Tyr Ser Leu Ala Val	
320	325	330
Ala Asp Leu Asn	Ser Asp Gly Trp Pro Asp Leu Ile Val Gly Ala	
335	340	345
Pro Tyr Phe Phe	Glu Arg Gln Glu Glu Leu Gly Gly Ala Val Tyr	
350	355	360
Val Tyr Leu Asn	Gln Gly Gly His Trp Ala Gly Ile Ser Pro Leu	
365	370	375
Arg Leu Cys Gly	Ser Pro Asp Ser Met Phe Gly Ile Ser Leu Ala	
380	385	390

Val Leu Gly Asp	Leu Asn Gln Asp Gly	Phe Pro Asp Ile Ala Val	395	400	405
Gly Ala Pro Phe	Asp Gly Asp Gly Lys	Val Phe Ile Tyr His Gly	410	415	420
Ser Ser Leu Gly	Val Val Ala Lys Pro	Ser Gln Val Leu Glu Gly	425	430	435
Glu Ala Val Gly	Ile Lys Ser Phe Gly	Tyr Ser Leu Ser Gly Ser	440	445	450
Leu Asp Met Asp	Gly Asn Gln Tyr Pro	Asp Leu Leu Val Gly Ser	455	460	465
Leu Ala Asp Thr	Ala Val Leu Phe Arg	Ala Arg Pro Ile Leu His	470	475	480
Val Ser His Glu	Val Ser Ile Ala Pro	Arg Ser Ile Asp Leu Glu	485	490	495
Gln Pro Asn Cys	Ala Gly Gly His Ser	Val Cys Val Asp Leu Arg	500	505	510
Val Cys Phe Ser	Tyr Ile Ala Val Pro	Ser Ser Tyr Ser Pro Thr	515	520	525
Val Ala Leu Asp	Tyr Val Leu Asp Ala	Asp Thr Asp Arg Arg Leu	530	535	540
Arg Gly Gln Val	Pro Arg Val Thr Phe	Leu Ser Arg Asn Leu Glu	545	550	555
Glu Pro Lys His	Gln Ala Ser Gly Thr	Val Trp Leu Lys His Gln	560	565	570
His Asp Arg Val	Cys Gly Asp Ala Met	Phe Gln Leu Gln Glu Asn	575	580	585
Val Lys Asp Lys	Leu Arg Ala Ile Val	Val Thr Leu Ser Tyr Ser	590	595	600
Leu Gln Thr Pro	Arg Leu Arg Arg Gln	Ala Pro Gly Gln Gly Leu	605	610	615
Pro Pro Val Ala	Pro Ile Leu Asn Ala	His Gln Pro Ser Thr Gln	620	625	630
Arg Ala Glu Ile	His Phe Leu Lys Gln	Gly Cys Gly Glu Asp Lys	635	640	645
Ile Cys Gln Ser	Asn Leu Gln Leu Val	His Ala Arg Phe Cys Thr	650	655	660
Arg Val Ser Asp	Thr Glu Phe Gln Pro	Leu Pro Met Asp Val Asp	665	670	675

Gly Thr Thr Ala Leu Phe Ala Leu Ser Gly Gln Pro Val Ile Gly	680	685	690
Leu Glu Leu Met Val Thr Asn Leu Pro Ser Asp Pro Ala Gln Pro	695	700	705
Gln Ala Asp Gly Asp Asp Ala His Glu Ala Gln Leu Leu Val Met	710	715	720
Leu Pro Asp Ser Leu His Tyr Ser Gly Val Arg Ala Leu Asp Pro	725	730	735
Ala Glu Lys Pro Leu Cys Leu Ser Asn Glu Asn Ala Ser His Val	740	745	750
Glu Cys Glu Leu Gly Asn Pro Met Lys Arg Gly Ala Gln Val Thr	755	760	765
Phe Tyr Leu Ile Leu Ser Thr Ser Gly Ile Ser Ile Glu Thr Thr	770	775	780
Glu Leu Glu Val Glu Leu Leu Leu Ala Thr Ile Ser Glu Gln Glu	785	790	795
Leu His Pro Val Ser Ala Arg Ala Arg Val Phe Ile Glu Leu Pro	800	805	810
Leu Ser Ile Ala Gly Met Ala Ile Pro Gln Gln Leu Phe Phe Ser	815	820	825
Gly Val Val Arg Gly Glu Arg Ala Met Gln Ser Glu Arg Asp Val	830	835	840
Gly Ser Lys Val Lys Tyr Glu Val Thr Val Ser Asn Gln Gly Gln	845	850	855
Ser Leu Arg Thr Leu Gly Ser Ala Phe Leu Asn Ile Met Trp Pro	860	865	870
His Glu Ile Ala Asn Gly Lys Trp Leu Leu Tyr Pro Met Gln Val	875	880	885
Glu Leu Glu Gly Gly Gln Gly Pro Gly Gln Lys Gly Leu Cys Ser	890	895	900
Pro Arg Pro Asn Ile Leu His Leu Asp Val Asp Ser Arg Asp Arg	905	910	915
Arg Arg Arg Glu Leu Glu Pro Pro Glu Gln Gln Glu Pro Gly Glu	920	925	930
Arg Gln Glu Pro Ser Met Ser Trp Trp Pro Val Ser Ser Ala Glu	935	940	945
Lys Lys Lys Asn Ile Thr Leu Asp Cys Ala Arg Gly Thr Ala Asn	950	955	960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Glu Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

gggtgacacc gcagtgcctc tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439

gttgetgggg actgcaatgt agct 24

<410> 440

<411> 46

<412> DNA

<413> Artificial Sequence

<420>

<423> Synthetic oligonucleotide probe

<430> 440

catccctccat gtctcccatg aggtctctat tgctccacga agcctc 46

<440> 441

<441> 1964

<442> DNA

<443> Homo sapiens

<450> 441

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agcagctcca gaaagcagcg agttggcaga gcagggtgc atttccagca 100
ggagctgaga gcacagtgtt ggctcacaac aagatgctca aggtgtcagc 150
cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200
cggcgggcgtt ggtgcagcc ggggggcggt cggacggcgg taattttctg 250
gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtgg 300
a cagtggaaac aaattccgag acgaagtaga ggatgattat ttccgcaatt 350
ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400
tgtttaaaga tgaaatgtag tgcgcataaa gtatgcattg ctcaagatto 450
tcagactgca gtctgcatta gtcacgggag gttacacac aggatgaaag 500
aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550
aagcagtgcc cagtggctca tcccagccct gtttgtggtt cagatggtea 600
tacctactct ttccagtga aactagaata tcaggcatgt gtcttaggaa 650
aacagatctc agtcaaatgt gaaggacatt gcccatgtcc ttcagataag 700
cccaccagta caagcagaaa tgttaagaga gcatgcagtg acctggagtt 750
caggggaagtg gcaaacagat tgcgggactg gttcaaggcc cttcatgaaa 800
gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850
agattcgata ccagcatctt gccaatctgc aaggactcac ttggctggat 900

gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950
 tcagaagcat ttaccttgat aagaatgaac agtgtacca ggcattcttc 1000
 aattcttgtg acacatacaa ggacagttta atatetaata atgagtgtg 1050
 ctactgcttc cagagacagc aagacccaac ttgccagaact gagctcagca 1100
 atattcagaa ggggcaaggg gtaagaagc tctaggaca gtatatccc 1150
 ctgtgtgatg aagatgggta ctacaagcca acacaatgtc atggcagtgt 1200
 tggacagtgc tgggtgtgtg acagatatgg aaatgaagtc atgggatcca 1250
 gaataaatgg tgttcagat tgtctatag attttgagat ctccggagat 1300
 tttgctagtg gcgattttca tgaatggact gatgatgagg atgatgaaga 1350
 cgatattatg aatgatgaag atgaaattga agatgatgat gaagatgaag 1400
 gggatgatga tgatgggtgt gatgacctg atgtatacat ttgattgatg 1450
 acagttgaaa tcaataaatt ctacatttct aatatttaca aaaatgatag 1500
 cctattttaa attatcttct tccccataa caaatgatt ctaaacctca 1550
 catatatttt gtataattat ttgaaaaatt gcagctaaag ttatagaact 1600
 ttatgtttta ataagaatca tttgctttga gtttttatat tccttacaca 1650
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 caaatgaca gctagtgttt gggatcgtac atgttaattt tttgaaagat 1800
 aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtctta 1850
 aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900
 ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950
 aaaaaaaaaa aaaa 1964

<210> 442
 <211> 436
 <212> PRT
 <213> Homo sapiens

<400> 442
 Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp
 1 5 10 15
 Cys Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly
 20 25 30
 Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu

	35	40	45
Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys	50	55	60
Phe Arg Asp Glu Val Glu Asp Asp Tyr Phe Arg Thr Trp Ser Pro	65	70	75
Gly Lys Pro Phe Asp Gln Ala Leu Asp Pro Ala Lys Asp Pro Cys	80	85	90
Leu Lys Met Lys Cys Ser Arg His Lys Val Cys Ile Ala Gln Asp	95	100	105
Ser Gln Thr Ala Val Cys Ile Ser His Arg Arg Leu Thr His Arg	110	115	120
Met Lys Glu Ala Gly Val Asp His Arg Gln Trp Arg Gly Pro Ile	125	130	135
Leu Ser Thr Cys Lys Gln Cys Pro Val Val Tyr Pro Ser Pro Val	140	145	150
Cys Gly Ser Asp Gly His Thr Tyr Ser Phe Gln Cys Lys Leu Glu	155	160	165
Tyr Gln Ala Cys Val Leu Gly Lys Gln Ile Ser Val Lys Cys Glu	170	175	180
Gly His Cys Pro Cys Pro Ser Asp Lys Pro Thr Ser Thr Ser Arg	185	190	195
Asn Val Lys Arg Ala Cys Ser Asp Leu Glu Phe Arg Glu Val Ala	200	205	210
Asn Arg Leu Arg Asp Trp Phe Lys Ala Leu His Glu Ser Gly Ser	215	220	225
Gln Asn Lys Lys Thr Lys Thr Leu Leu Arg Pro Glu Arg Ser Arg	230	235	240
Phe Asp Thr Ser Ile Leu Pro Ile Cys Lys Asp Ser Leu Gly Trp	245	250	255
Met Phe Asn Arg Leu Asp Thr Asn Tyr Asp Leu Leu Leu Asp Gln	260	265	270
Ser Glu Leu Arg Ser Ile Tyr Leu Asp Lys Asn Glu Gln Cys Thr	275	280	285
Lys Ala Phe Phe Asn Ser Cys Asp Thr Tyr Lys Asp Ser Leu Ile	290	295	300
Ser Asn Asn Glu Trp Cys Tyr Cys Phe Gln Arg Gln Gln Asp Pro	305	310	315
Pro Cys Gln Thr Glu Leu Ser Asn Ile Gln Lys Arg Gln Gly Val			

	320		325		330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro Leu Cys Asp Glu Asp Gly					
	335		340		345
Tyr Tyr Lys Pro Thr Gln Cys His Gly Ser Val Gly Gln Cys Trp					
	350		355		360
Cys Val Asp Arg Tyr Gly Asn Glu Val Met Gly Ser Arg Ile Asn					
	365		370		375
Gly Val Ala Asp Cys Ala Ile Asp Phe Glu Ile Ser Gly Asp Phe					
	380		385		390
Ala Ser Gly Asp Phe His Glu Trp Thr Asp Asp Glu Asp Asp Glu					
	395		400		405
Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu Asp Asp Asp Glu					
	410		415		420
Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His Asp Val Tyr					
	425		430		435
Ile					

<210> 443

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

caagaatatt cagaagcggc aaggg 25

<210> 444

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

catcatggtc atcaccacca tcatcatc 28

<210> 445

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgacatgga agtgttggaa agt atgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

caaacacag atttccctgt caaacacag gagtcacag aggaacacag 50
gagcggagac aacagtaact aacgcctctt tcagcccgag atcacccag 100
cagggatggg cgacaagatc tggctgacct tccccgtgt cttctgtgac 150
gtcttgcttc cggctgtgtg gctcggggcg gcgggcttca cacttccct 200
cgatagcgac ttacacctta ccttcccgcc cggccagaag gactccttct 250
accagcccat gccctgaag gccctgctgg agatcgagta ccaactttta 300
gatcggcag gattagatat ttatttcctt ctgcctctc cagaaggcaa 350
aaccttagtt ttgaacaaa gaaatcaga tggagttcct actgtagaaa 400
ctgagtttgg tgattacatg ttctgttttg acaatacatt cagcaccatt 450
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ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550
tggatatgaa actggaagac atcctggaat ccaccaacag catcaagtc 600
agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc 650
tcgtgacgca aacatacaag aaagcaactt tgatagagtc aatttctggt 700
ctatggttaa tttagtggtc atggctgggtg tgtcagccat tcaagtttat 750
atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaactc 800
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tgttacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900
aaagtaggaa acaggtataa ttttaatgtg aaaattaagt cttcactttc 950
tgtgcaagta atcctgctga tcagcttga ctttaagtgt taacaggaat 1000
attttgcaga atataggttt aactgaatga agccatatta ataactgcac 1050
tttccaaact ttgaaaaatt ttgcaaatgt cttaggtgat ttaaataaat 1100
gaglattggg cctaattgca acaccagtct gtttttaaca ggttctatta 1150
cccagaactt ttttglaaat ggggcagtta caaattaact gtggaagttt 1200
tcagttttta gttataaate aactgagaat tacctaataa tggattgaat 1250

aaatcttttag actacaaaag cccaactttt ctctatttac atatgcattc 1300
ctctataat gtaaatagaa taatagcttt gaaatacaat taggtttttg 1350
agattttttat aaccaaatac atttcagtgt aacatattag cagaaagcat 1400
tagtcittgt actttgctta cattcccaaa agctgacatt ttcaagatte 1450
ttaaaaacac aaagttacac ttactaaaat taggacatgt tttctctttg 1500
aatgaagaa tatagtttaa aagcttctc ctccataggg acacattttc 1550
tctaaccctt aactaaagt taggatttta aaattaaatg tgaggtaaaa 1600
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taaataaata tctccttttc tgagctctaa gaattatcag aaaacaggaa 1800
agaatttaga aaaacttgag aaaacctaat ccaaaaataaa attcattaa 1850
gtagaactat aaataaatat ctagaatctg actggctcat catgacatcc 1900
tactcataac ataaatcaaa ggagatgatt aatttccagt tagctggaag 1950
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gaaacataga ctccaagtt ttaaaccact aaatgtgaat aacctatata 2200
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 gtacaataat gcacaatcag tgttgctcaa actgctttat acttataaac 3550
 agccatctta aataagcaac gtattgtgag tactgatatg tatataataa 3600
 aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

Met	Gly	Asp	Lys	Ile	Trp	Leu	Pro	Phe	Pro	Val	Leu	Leu	Leu	Ala
1				5					10					15

Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30

Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45

Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His	65	70	75
Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys	80	85	90
Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met	95	100	105
Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile	110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu	125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp	140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser	155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe	170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val	185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser	200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	215	220	225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

cccagcaggg ctgggcgaca aga 23

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gttttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<222> Synthetic oligonucleotide probe

<400> 450

ccaaaaggag cacggggaag ggcagccaga ttttgtegcc cat 43

<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

ccatccctga gatcttttta taaaaaaccc agtctttgct gaccagacaa 50

agcataccag atctcaccag agagtcgcag acactatgct gctcccatg 100

gccttgccca gtgtgtcctg gatgctgctt tcttgctca ttctcctgtg 150

tcagggttcaa ggtgaagaaa ccagaagga actgcctct ccacggatca 200

gctgtcccaa aggcctcaag gctatggtt cccctgcta tgccttgttt 250

ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300

ctctggaaaa ctggtgtctg tgcctcagtg ggctgaggga tcttcgtgt 350

cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400

ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450

gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500

ccatcttaaa ccttgccac tgtgggagcc tgtcaagaag cacaggattt 550

ctgaagtggc aagattataa ctgtgatgca aagttaccct atgtctgcaa 600

gttcaaggac tagggcaggt gggaagtcag cagcctcagc ttggcgtgca 650

gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700

ttctccccc aa actgcctac ctgactacct tgtcatgac ctctttcttt 750

ttcttttttc ttaccttca ttccaggctt ttctctgtct tccatgtctt 800

aggtctcag agaataataa taaaaatgtt actttataaa aaaaaaaaaa 850

aaaaaaaaa 859

<210> 452

<211> 175

<210> PRT
<213> Homo sapiens

<400> 452

Met	Leu	Pro	Pro	Met	Ala	Leu	Pro	Ser	Val	Ser	Trp	Met	Leu	Leu	
1				5					10					15	
Ser	Cys	Leu	Ile	Leu	Leu	Cys	Gln	Val	Gln	Gly	Glu	Alu	Thr	Gln	
			20						25					30	
Lys	Glu	Leu	Pro	Ser	Pro	Arg	Ile	Ser	Cys	Pro	Lys	Gly	Ser	Lys	
			35						40					45	
Ala	Tyr	Gly	Ser	Pro	Cys	Tyr	Ala	Leu	Phe	Leu	Ser	Pro	Lys	Ser	
			50						55					60	
Trp	Met	Asp	Ala	Asp	Leu	Ala	Cys	Gln	Lys	Arg	Pro	Ser	Gly	Lys	
			65						70					75	
Leu	Val	Ser	Val	Leu	Ser	Gly	Ala	Glu	Gly	Ser	Phe	Val	Ser	Ser	
			80						85					90	
Leu	Val	Arg	Ser	Ile	Ser	Asn	Ser	Tyr	Ser	Tyr	Ile	Trp	Ile	Gly	
			95						100					105	
Leu	His	Asp	Pro	Thr	Gln	Gly	Ser	Glu	Pro	Asp	Gly	Asp	Gly	Trp	
			110						115					120	
Glu	Trp	Ser	Ser	Thr	Asp	Val	Met	Asn	Tyr	Phe	Ala	Trp	Glu	Lys	
			125						130					135	
Asn	Pro	Ser	Thr	Ile	Leu	Asn	Pro	Gly	His	Cys	Gly	Ser	Leu	Ser	
			140						145					150	
Arg	Ser	Thr	Gly	Phe	Leu	Lys	Trp	Lys	Asp	Tyr	Asn	Cys	Asp	Ala	
			155						160					165	
Lys	Leu	Pro	Tyr	Val	Cys	Lys	Phe	Lys	Asp						
			170						175						

<210> 453

<211> 550

<212> ENA

<213> Homo sapiens

<400> 453

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ggcgtctctg gcgctggtgc tggctgctg cggagagctg gcgcgggccc 150
tgcgtctgta cgtctgtccg gaggccacag gactgtcgga ctgtgtcacc 200
atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250
ccgggagata gtgtaccctc tccaggggga ctccaagggtg accaagtcct 300

gtgccagcaa gtgtaagccc tgggatgtgg atggcatcgg ccagaccctg 350
 cccgtgtcct gctgcaatac tgagctgtgc aatgtagaag gggcgaccgc 400
 tctgaacagc ctccactgag gggccctcac gctcctccca ctcttgagcc 450
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 <211> 125
 <212> PRT
 <213> Homo sapiens

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 Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr
 35 40 45
 Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val
 50 55 60
 Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser
 65 70 75
 Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro
 80 85 90
 Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro
 95 100 105
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 110 115 120
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 <211> 1518
 <212> DNA
 <213> Homo sapiens

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 aataagtacc agaccattga caactaccag ccgtaccctg ggcagagga 400
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 ctgaaagctt tggtaatgat catagccctc tggatgggta ttccagaaga 650
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<210> 456

<211> 266

<212> FRT

<213> Homo sapiens

<400> 456

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				20					25					30
Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu
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Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val
				50					55					60
Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln
				65					70					75
Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Gln
				80					85					90
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp
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Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg
				110					115					120
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn
				125					130					135
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile
				140					145					150
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu
				155					160					165
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His
				170					175					180
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys
				185					190					195
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys
				200					205					210
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg
				215					220					225
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly
				230					235					240
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser
				245					250					255
Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His				
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<211> 638
<212> DNA
<213> Homo sapiens

<220>
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509, 556
<223> unknown base

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<211> 4040
<212> DNA
<213> Homo sapiens

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cattgaaaag aagagaattt gatgctgctg ttaattctgg agaactgigg 850
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 <211> 747
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ala Ser Ser Arg Glu Ile Arg Gln Ala Phe Lys Lys Leu Ala Leu
 50 55 60
 Lys Leu His Pro Asp Lys Asn Pro Asn Asn Pro Asn Ala His Gly
 65 70 75

Arg	Phe	Leu	Lys	Ile	Asn	Arg	Ala	Tyr	Glu	Val	Leu	Lys	Asp	Glu	80	85	90
Asp	Leu	Arg	Lys	Lys	Tyr	Asp	Lys	Tyr	Gly	Glu	Lys	Gly	Leu	Glu	95	100	105
Asn	Asn	Gln	Gly	Gly	Gln	Tyr	Glu	Ser	Trp	Asn	Tyr	Tyr	Arg	Tyr	110	115	120
Asp	Phe	Gly	Ile	Tyr	Asp	Asp	Asp	Pro	Glu	Ile	Ile	Thr	Leu	Glu	125	130	135
Arg	Arg	Glu	Phe	Asp	Ala	Ala	Val	Asn	Ser	Gly	Glu	Leu	Trp	Phe	140	145	150
Val	Asn	Phe	Tyr	Ser	Pro	Gly	Cys	Ser	His	Cys	His	Asp	Leu	Ala	155	160	165
Pro	Thr	Trp	Arg	Asp	Phe	Ala	Lys	Glu	Val	Asp	Gly	Leu	Leu	Arg	170	175	180
Ile	Gly	Ala	Val	Asn	Cys	Gly	Asp	Asp	Arg	Met	Leu	Cys	Arg	Met	185	190	195
Lys	Gly	Val	Asn	Ser	Tyr	Pro	Ser	Leu	Phe	Ile	Phe	Arg	Ser	Gly	200	205	210
Met	Ala	Pro	Val	Lys	Tyr	His	Gly	Asp	Arg	Ser	Lys	Glu	Ser	Leu	215	220	225
Val	Ser	Phe	Ala	Met	Gln	His	Val	Arg	Ser	Thr	Val	Thr	Glu	Leu	230	235	240
Trp	Thr	Gly	Asn	Phe	Val	Asn	Ser	Ile	Gln	Thr	Ala	Phe	Ala	Ala	245	250	255
Gly	Ile	Gly	Trp	Leu	Ile	Thr	Phe	Cys	Ser	Lys	Gly	Gly	Asp	Cys	260	265	270
Leu	Thr	Ser	Gln	Thr	Arg	Leu	Arg	Leu	Ser	Gly	Met	Leu	Phe	Leu	275	280	285
Asn	Ser	Leu	Asp	Ala	Lys	Glu	Ile	Tyr	Leu	Glu	Val	Ile	His	Asn	290	295	300
Leu	Pro	Asp	Phe	Glu	Leu	Leu	Ser	Ala	Asn	Thr	Leu	Glu	Asp	Arg	305	310	315
Leu	Ala	His	His	Arg	Trp	Leu	Leu	Phe	Phe	His	Phe	Gly	Lys	Asn	320	325	330
Glu	Asn	Ser	Asn	Asp	Pro	Glu	Leu	Lys	Lys	Leu	Lys	Thr	Leu	Leu	335	340	345
Lys	Asn	Asp	His	Ile	Gln	Val	Gly	Arg	Phe	Asp	Cys	Ser	Ser	Ala	350	355	360

Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala	365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly	380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val	395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn	410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro	425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu	440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His	455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr	470	475	480
Val Val Phe Asn Gln Ser Asn Ile His Gln Tyr Glu Gly His His	485	490	495
Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro	500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr	515	520	525
Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro	530	535	540
Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met	545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys	560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr	575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln	590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg	605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr	620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp	635	640	645

Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe
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Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val
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Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln
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Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr
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Glu	Arg	Ala	Lys	Arg	Asn	Ile	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg
				710					715					720

Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 461
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 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 461
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<210> 462
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 462
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<210> 463
 <211> 1818
 <212> DNA

<213> Homo sapiens

<400> 463

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 atggacccaa gagaaga 1818

<210> 464
 <211> 300
 <212> PRT
 <213> Homo sapiens

<400> 464
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 Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg
 20 25 30
 Arg Lys Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly
 35 40 45
 His Gly Ile Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln
 50 55 60
 Ser Ile Leu Val Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu
 65 70 75
 Thr Ala Ala Glu Cys Arg Lys Leu Gly Val Thr Ala His Ala Tyr
 80 85 90
 Val Val Asp Cys Ser Asn Arg Glu Glu Ile Tyr Arg Ser Leu Asn
 95 100 105
 Gln Val Lys Lys Glu Val Gly Asp Val Thr Ile Val Val Asn Asn
 110 115 120
 Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr Lys Asp Glu
 125 130 135
 Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His Phe Trp
 140 145 150
 Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His Gly

155	160	165
His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro		
170	175	180
Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe		
185	190	195
His Arg Gly Leu Thr Ser Gln Leu Gln Ala Leu Gly Lys Thr Gly		
200	205	210
Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe		
215	220	225
Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp		
230	235	240
Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys		
245	250	255
Met Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln		
260	265	270
Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln		
275	280	285
Asn Ile Gln Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys		
290	295	300

<210> 465

<211> 1547

<212> DNA

<213> Homo sapiens

<100> 465

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gagagggccc agcccgcccc gggcaggatg accaaggccc ggctgttccg 150

gctgtggctg gtgctggggg cgggtgttcac gatcctgctg atcatcgtgt 200

actgggacag cgcaggcgcc gcgcacttct acttgacac gtccttctct 250

aggccgcaca cggggcgccc gctgcccacg cccgggcccg acagggacag 300

ggagctcacg gccgaactcg atgtcgacga gtttctggac aagtttctca 350

gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccc 400

cctgggcggg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450

ggcgacgcc cggcgcgccc cagaccaggg ccggcagcag gggagcgga 500

ggagcgtgct ggggggcttc tgccccaact ccagcctggc ctccccacc 550

aaggagcgcg cattcgaaga catccccaac tcggagctga gccacctgat 600
cgtggacgac cggcacgggg ccattctactg ctacttgccc aaggtggcct 650
gcaccaactg gaagcgcgtg atgategtgc tgagcgggaag cctgctgcac 700
cggggtgcgc ctaccgcga cccgatgcgc atccgcgcgc agcacgtgca 750
caacgcagc ggcacactga ccttcacaaa gttctggcgc cgtacggga 800
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ctcttcgtgc ggcacccctt cgtgcgcctg atctccgcct tcgcagcaa 900
gttcgagctg gagaacgagg agttctacgc caagttcgcc gtgcccctgc 950
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tgtaccgct ctgcacccgc tgcagatgc actacgactt cgtggggaag 1150
ctggagactc tggacgagga cgcgcgcag ctgctgcagc tactccaggt 1200
ggacgggcag ctccgcttcc ccccgagcta ccggaacagg accgcacga 1250
gctgggagga ggaactggtc gccaaagatcc cctggcctg gaggcagcag 1300
ctgtataaac tctacgagge cgactttggt ctcttcggct accccaagcc 1350
cgaaaaactc ctccgagact gaaagcttcc gcgttgcttt ttctcgcgtg 1400
cctggaaact gacgcacgcg cactccagtt ttttatgac ctacgatttt 1450
gcaatctggg cttcttggtc actccactgc ctctatccat tgagtactgt 1500
atcgatattg ttttttaaga ttaatatatt tcaggtattt aatacga 1547

#E10: 466
#E11: 414
#E12: PRT
#E13: Homo sapiens

#A00: 466
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Val Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly
20 25 30
Ala Ala His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr
35 40 45
Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu
50 55 60

Thr	Ala	Asp	Ser	Asp	Val	Asp	Glu	Phe	Leu	Asp	Lys	Phe	Leu	Ser	65	70	75
Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro	Arg	Lys	Glu	Thr	Glu	Gln	80	85	90
Pro	Pro	Ala	Pro	Gly	Ser	Met	Glu	Glu	Ser	Val	Arg	Gly	Tyr	Asp	95	100	105
Trp	Ser	Pro	Arg	Asp	Ala	Arg	Arg	Ser	Pro	Asp	Gln	Gly	Arg	Gln	110	115	120
Gln	Ala	Glu	Arg	Arg	Ser	Val	Leu	Arg	Gly	Phe	Cys	Ala	Asn	Ser	125	130	135
Ser	Leu	Ala	Phe	Pro	Thr	Lys	Glu	Arg	Ala	Phe	Asp	Asp	Ile	Pro	140	145	150
Asn	Ser	Glu	Leu	Ser	His	Leu	Ile	Val	Asp	Asp	Arg	His	Gly	Ala	155	160	165
Ile	Tyr	Cys	Tyr	Val	Pro	Lys	Val	Ala	Cys	Thr	Asn	Trp	Lys	Arg	170	175	180
Val	Met	Ile	Val	Leu	Ser	Gly	Ser	Leu	Leu	His	Arg	Gly	Ala	Pro	185	190	195
Tyr	Arg	Asp	Pro	Leu	Arg	Ile	Pro	Arg	Glu	His	Val	His	Asn	Ala	200	205	210
Ser	Ala	His	Leu	Thr	Phe	Asn	Lys	Phe	Trp	Arg	Arg	Tyr	Gly	Lys	215	220	225
Leu	Ser	Arg	His	Leu	Met	Lys	Val	Lys	Leu	Lys	Lys	Tyr	Thr	Lys	230	235	240
Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe	245	250	255
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe	260	265	270
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro	275	280	285
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe	290	295	300
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu	305	310	315
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His	320	325	330
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu	335	340	345

Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg
			350					355						360
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser
			365					370						375
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln
			380					385						390
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr
			395					400						405
Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp						
			410											

<210> 467
 <211> 1971
 <212> DNA
 <213> Homo sapiens

<400> 467
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 aggggatggc taagggaacg cgtatgccc ggaaggtggt ggtcgtgacc 150
 gggggcgggc ggggcacgg agctgggata gtggcgccct tcgtgaacag 200
 aggggcctga gtgggttatct ggcacaagga tgagtctggg ggccggggcc 250
 tggagcagga gctccctgga gctgtcttta tctctgtga tgtgactcag 300
 gaagatgatg tgaagaccc ggtttctgag accatccgcc gatttgcccg 350
 cctggattgt gttgtcaaca accgtggcca ccacccaccc ccacagaggg 400
 ctgaggagac ctctgccag ggattccgcc agctgtgga gctgaacctc 450
 ctggggacgt acaccttgac caagctcgcc ctccctaac tgagggaagag 500
 tcaaggggat gtcataaca tctccagcct ggtgggggca atcgccagg 550
 ccagggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600
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 ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700
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 ggcgcctggt gccagccccc tgaggctggg gctggggcag tgttccctgg 800
 ctccgaagcc aacttctgca cgggcattga actgctcgtg acgggggggtg 850
 cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900

cccgatatcc ctctctgatt tctctcattt ctacttgggg ccccttccct 950
 aggaactctcc caaccccaaac tccaacctgt atcaqatgca gccccaagc 1000
 ccttagactc taagccaggt tagcaagggtg ccgggtcacc ctgcaggttc 1050
 ccataaaaac gatttgagc c 1071

<210> 468
 <211> 270
 <212> P5T
 <213> Homo sapiens

<400> 468
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 20 25 30
 Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly
 35 40 45
 Gly Arg Ala Leu Gln Gln Glu Leu Pro Gly Ala Val Phe Ile Leu
 50 55 60
 Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu
 65 70 75
 Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala
 80 85 90
 Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln
 95 100 105
 Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr
 110 115 120
 Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn
 125 130 135
 Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln
 140 145 150
 Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr
 155 160 165
 Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn
 170 175 180
 Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu
 185 190 195
 Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met
 200 205 210

Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly
				215					220					225
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
				230					235					240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys
				245					250					255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser
				260					265					270

<210> 469
 <211> 687
 <212> DNA
 <213> Homo sapiens

<300> 409
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 actcaaac accgtgtttct tcttaccatt tcatcttcc tggggctggg 100
 ccagcccagg agccccaaaa gcaagaggaa ggggcaagg cggcctgggc 150
 cccctggccc tggccctcac caggtgcac tggacctggt gtcacggatg 200
 aaacctatg cccgcctgga ggagtatgag aggaacatcg aggagatggt 250
 agcccagctg aggaacagct cagagcttgc ccagagaaaag tgtgaggtca 300
 acttgcagct gtggatgtcc aacaagagga gctgtctcc ctggggctac 350
 agctcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400
 gtgcctgtgt ctgggtgtgt tgaacccctt caacctgcag gaggacggca 450
 acatggtgag cgtgcgggtg ttcagccagg ttcctgtgag ccgcgcctc 500
 tgcctgcac cgcctccgac agggccttgc cgcagcgcg cagtcatgga 550
 gacctcgct gtgggtgca cctgcattt ctgaatcac tggcccagaa 600
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 ggcatatgaa aagtaaacac tgacttttga aagcaag 687

<310> 470
 <311> 180
 <312> PRT
 <313> Homo sapiens

Met	Asp	Trp	Pro	His	Asn	Leu	Leu	Phe	Leu	Leu	Thr	Ile	Ser	Ile
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Phe	Leu	Gly	Leu	Gly	Gln	Pro	Arg	Ser	Pro	Lys	Ser	Lys	Arg	Lys
				20					25					30

Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val
				35					40					45
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu
				50					55					60
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn
				65					70					75
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu
				80					85					90
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile
				95					100					105
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg
				110					115					120
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp
				125					130					135
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg
				140					145					150
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln
				155					160					165
Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe
				170					175					180

<210> 471
 <211> 2368
 <212> DNA
 <213> Homo sapiens

<400> 471
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 ctcccccgcg agaagcctcg ctggggcgcc aacatggcgg gtggggcgctg 150
 cggcccgag ctaaaggcgc tctggcgccg ctggatcgcg gctgtggcgg 200
 cgaaggcagg ccccgaggag gcgcgctgc cgcggagca gagccgggtc 250
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 gctgaaattt taagcccat ggtgtccatc ctgcccagcag actgattcag 350
 aatggggagg ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400
 aaggtagatg tcattcaaga accaggtttg agtggccgct tctttgtcac 450
 cactctccca gcatTTTTTc atgcaaagga tgggatatto cgcggttato 500

gtggcccagg aatcttcgaa gacctgcaga attatatctt agagaagaaa 550
tggaatcag tcagactct gactggetg aaatcccag cttctctaac 600
catgtctgga atggctggtc tttttagcat ctctggcaag atatggcctc 650
ttcacaacta tttcacagt gctcttggaa ttctgcttg gtgtttctat 700
gtgttttttg tcatagccac cttggttttt ggccttttta tgggtctggt 750
cttggtggtt atatcagaat gttcttatgt gcaacttca aggcatttat 800
ctgagcgttc tgagcagaat cggagatcag aggaggctca tagagctgaa 850
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gatgaggaga gaagtgggc caatgatcag gggcccacag gagaggacgg 1050
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cgtaaaagtc agcatctga caagggactg tagatttaat gatgcgtttt 1200
caagaataca caaaaaaca atatgtcagc ttcccttgg cctgcagttt 1250
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gatctgtttg gagaactggga tgggaacaag ttcatttaac taggggtcag 1450
agagtctcga ccagaggagg ccattcccag tctaatacag caocttcacg 1500
agacaaggct gcaggccctg tgaaatgaaa gccaaagcag agccttggct 1550
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atgaaaaatc tttcacagct agaaattgaa agggccttgg gtatagagag 1700
cagctcagaa gtcaccccag cctctgaat ctctgtgct atgttttatt 1750
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taaccataac cctgaagct gtgactgcca aacatctcaa atgaaatgtt 1950

gtggccatca gagactcaaa aggaagtaag gattttacaa gacagattaa 2000
 aaaaaaattg ttttgtccaa aatatagttg ttgttgattt ttttttaagt 2050
 ttttataagca atatttttca agccagaagt cctctaagtc ttgccagtac 2100
 aaggtagtct tgtgaagaaa agttgaatac tgttttgttt tcattctaaag 2150
 gggttccctg ggtcttgaac tactttaata ataactaaaa aaccacttct 2200
 gatttttcctt cagtgatgtg cttttggtga aagaattaat gaactccagt 2250
 acctgaaagt gaaagatttg attttgtttc catctttctgt aatcttccaa 2300
 agaatttatat ctttgtaaat ctctcaatac tcaatctact gtaagtaccc 2350
 agggagagcta atttcttt 2368

<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

Met	Ala	Gly	Gly	Arg	Cys	Gly	Pro	Gln	Leu	Thr	Ala	Leu	Leu	Ala	1	5	10	15
Ala	Trp	Ile	Ala	Ala	Val	Ala	Ala	Thr	Ala	Gly	Pro	Glu	Glu	Ala	20	25	30	
Ala	Leu	Pro	Pro	Glu	Gln	Ser	Arg	Val	Gln	Pro	Met	Thr	Ala	Ser	35	40	45	
Asn	Trp	Thr	Leu	Val	Met	Glu	Gly	Glu	Trp	Met	Leu	Lys	Phe	Tyr	50	55	60	
Ala	Pro	Trp	Cys	Pro	Ser	Cys	Gln	Gln	Thr	Asp	Ser	Glu	Trp	Glu	65	70	75	
Ala	Phe	Ala	Lys	Asn	Gly	Glu	Ile	Leu	Gln	Ile	Ser	Val	Gly	Lys	80	85	90	
Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val	95	100	105	
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg	110	115	120	
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile	125	130	135	
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys	140	145	150	
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser	155	160	165	

Ile Ser Gly Lys Ile Trp His Leu His Asn Tyr Phe Thr Val Thr
170 175 180

Leu Gly Ile Pro Ala Trp Cys Ser Tyr Val Phe Phe Val Ile Ala
185 190 195

Thr Leu Val Phe Gly Leu Phe Met Gly Leu Val Leu Val Val Ile
200 205 210

Ser Glu Cys Phe Tyr Val Pro Leu Pro Arg His Leu Ser Glu Arg
215 220 225

Ser Glu Gln Asn Arg Arg Ser Glu Glu Ala His Arg Ala Glu Gln
230 235 240

Leu Gln Asp Ala Glu Glu Glu Lys Asp Asp Ser Asn Glu Glu Glu
245 250 255

Asn Lys Asp Ser Leu Val Asp Asp Glu Glu Glu Lys Glu Asp Leu
260 265 270

Gly Asp Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Asp Asn Leu
275 280 285

Ala Ala Gly Val Asp Glu Glu Arg Ser Glu Ala Asn Asp Gln Gly
290 295 300

Pro Pro Gly Glu Asp Gly Val Thr Arg Glu Glu Val Glu Pro Glu
305 310 315

Gln Ala Glu Glu Gly Ile Ser Glu Gln Pro Cys Pro Ala Asp Thr
320 325 330

Glu Val Val Glu Asp Ser Leu Arg Gln Arg Lys Ser Gln His Ala
335 340 345

Asp Lys Gly Leu

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<225> Synthetic oligonucleotide probe

<400> 473

gtccagccca tgaccgcctc caac 24

<210> 474

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

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<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

gtggatgctg aaattttlacg ccccatggcg tccatcctgc cagc 44

<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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gcacacatga tttagctcag agattctctt ttgtccacag acagtcctct 100

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tcaagaacaa tggaaatatc tctgattta gaaaatttgg atgaagatgg 200

atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250

tttcagagaa aggatcgtgt gctgcctctc ctccctggcg cctcattgct 300

gtaattttgg gaatcctatg cttggtaata ctggtgatag ctgtggctct 350

gggtaccatg ggggttcttt ccagcccttg tctcctaatt tggattatat 400

atgagaagag ctgttatcta ttcagcatgt cactaaatc ctgggatgga 450

agtaaaagac aatgctggca actgggctct aatctcctaa agatagacag 500

ctcaaatgaa ttgggattta tagtaaaaca agtgtcttcc caacctgata 550

attcattttg gataggcctt tctgggcccc agactgaggt accatggctc 600

tgggaggatg gatcaacatt ctctttctaac ttatttcaga tcagaaccac 650

agtaacccaa gaaaaccat ctcccaattg tgtatggatt caagtgtcag 700

tcatttatga ccaactgtgt agtgtgcctt catatagtat ttgtgagaag 750

aagttttcaa tgtaagagga aggggtggaga aggagagaga aatatgtgag 800

gtagtaagga ggacagaaaa cagaacagaa aagagtaaca gctgagggtc 850

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 <212> FRT
 <213> Homo sapiens

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 Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile
 50 55 60
 Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro
 65 70 75
 Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met
 80 85 90
 Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu
 95 100 105
 Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe
 110 115 120
 Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile
 125 130 135
 Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp
 140 145 150
 Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala
 155 160 165
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<213> Artificial Sequence

<220>
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<400> 480
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 <211> 693
 <212> PRT
 <213> Homo sapiens

<210> 483
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 Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser
 35 40 45
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn
 50 55 60
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His
 65 70 75
 Pro Ala Ser Arg Ser Phe Pro Asp Pro Arg Gly Leu Tyr His Phe
 80 85 90

Cys Leu Tyr Trp Asn Arg His Ala Gly Arg Leu His Leu Leu Tyr	95	100	105
Gly Lys Arg Asp Phe Leu Leu Ser Asp Lys Ala Ser Ser Leu Leu	110	115	120
Cys Phe Gln His Gln Glu Glu Ser Leu Ala Gln Gly Pro Pro Leu	125	130	135
Leu Ala Thr Ser Val Thr Ser Trp Trp Ser Pro Gln Asn Ile Ser	140	145	150
Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser Phe His Ser Pro Pro	155	160	165
His Thr Ala Ala His Asn Ala Ser Val Asp Met Cys Glu Leu Lys	170	175	180
Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His Pro Gln Lys	185	190	195
Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln Leu Gln	200	205	210
Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp Met	215	220	225
Val Ser Phe Glu Gln Asp Arg Ile Asn Ala Thr Val Trp Lys Leu	230	235	240
Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln	245	250	255
Glu Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro	260	265	270
Arg Thr Leu Phe Gln Arg Thr Lys Gly Arg Ser Gly Glu Ala Glu	275	280	285
Lys Arg Leu Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln	290	295	300
Asp Lys Asn Ser Ser Gln Val Leu Gly Glu Lys Val Leu Gly Ile	305	310	315
Val Val Gln Asn Thr Lys Val Ala Asn Leu Thr Glu Pro Val Val	320	325	330
Leu Thr Phe Gln His Gln Leu Gln Pro Lys Asn Val Thr Leu Gln	335	340	345
Cys Val Phe Trp Val Glu Asp Pro Thr Leu Ser Ser Pro Gly His	350	355	360
Trp Ser Ser Ala Gly Cys Glu Thr Val Arg Arg Glu Thr Gln Thr	365	370	375

Ser	Cys	Phe	Cys	Asn	His	Leu	Thr	Tyr	Phe	Ala	Val	Leu	Met	Val	380	390
Ser	Ser	Val	Glu	Val	Asp	Ala	Val	His	Lys	His	Tyr	Leu	Ser	Leu	395	405
Leu	Ser	Tyr	Val	Gly	Cys	Val	Val	Ser	Ala	Leu	Ala	Cys	Leu	Val	410	420
Thr	Ile	Ala	Ala	Tyr	Leu	Cys	Ser	Arg	Val	Pro	Leu	Pro	Cys	Arg	425	435
Arg	Lys	Pro	Arg	Asp	Tyr	Thr	Ile	Lys	Val	His	Met	Asn	Leu	Leu	440	450
Leu	Ala	Val	Phe	Leu	Leu	Asp	Thr	Ser	Phe	Leu	Leu	Ser	Glu	Pro	455	465
Val	Ala	Leu	Thr	Gly	Ser	Glu	Ala	Gly	Cys	Arg	Ala	Ser	Ala	Ile	470	480
Phe	Leu	His	Phe	Ser	Leu	Leu	Thr	Cys	Leu	Ser	Trp	Met	Gly	Leu	485	495
Glu	Gly	Tyr	Asn	Leu	Tyr	Arg	Leu	Val	Val	Glu	Val	Phe	Gly	Thr	500	510
Tyr	Val	Pro	Gly	Tyr	Leu	Leu	Lys	Leu	Ser	Ala	Met	Gly	Trp	Gly	515	525
Phe	Pro	Ile	Phe	Leu	Val	Thr	Leu	Val	Ala	Leu	Val	Asp	Val	Asp	530	540
Asn	Tyr	Gly	Pro	Ile	Ile	Leu	Ala	Val	His	Arg	Thr	Pro	Glu	Gly	545	555
Val	Ile	Tyr	Pro	Ser	Met	Cys	Trp	Ile	Arg	Asp	Ser	Leu	Val	Ser	560	570
Tyr	Ile	Thr	Asn	Leu	Gly	Leu	Phe	Ser	Leu	Val	Phe	Leu	Phe	Asn	575	585
Met	Ala	Met	Leu	Ala	Thr	Met	Val	Val	Gln	Ile	Leu	Arg	Leu	Arg	590	600
Pro	His	Thr	Gln	Lys	Trp	Ser	His	Val	Leu	Thr	Leu	Leu	Gly	Leu	605	615
Ser	Leu	Val	Leu	Gly	Leu	Pro	Trp	Ala	Leu	Ile	Phe	Phe	Ser	Phe	620	630
Ala	Ser	Gly	Thr	Phe	Gln	Leu	Val	Val	Leu	Tyr	Leu	Phe	Ser	Ile	635	645
Ile	Thr	Ser	Phe	Gln	Gly	Phe	Leu	Ile	Phe	Ile	Trp	Tyr	Trp	Ser	650	660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn
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Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser
680 685 690

Ser Arg Ile

<210> 484
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 64, 70, 84, 147
<223> unknown base

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<210> 485
<211> 52
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<300> 485
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<210> 486
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<212> DNA

<213> Artificial Sequence

<215>

<213> Synthetic oligonucleotide probe

<400> 436

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<210> 437

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<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2715

<223> unknown base

<400> 487

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<210> 438

<211> 345

<212> PRT

<213> Homo sapiens

<400> 438

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Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln
				35					40					45
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser
				50					55					60
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp
				65					70					75
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe
				80					85					90
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys
				95					100					105
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu
				110					115					120
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser
				125					130					135
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe
				140					145					150
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro
				155					160					165

Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala	170	175	180
Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr	185	190	195
Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu	200	205	210
Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys	215	220	225
Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu	230	235	240
Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe	245	250	255
Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe	260	265	270
Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala	275	280	285
Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys	290	295	300
Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr	305	310	315
Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu	320	325	330
His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly	335	340	345

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4010 491

4011 20

4012 DNA

4013 Artificial Sequence

4020

4021 Synthetic oligonucleotide probe

4030 491

4031 atctatagcg tttaaccagg 20

4040 492

4041 20

4042 DNA

4043 Artificial Sequence

4050

4051 Synthetic oligonucleotide probe

4060 492

4061 atctcagca cagttccac 20

4070 493

4071 21

4072 DNA

4073 Artificial Sequence

4080

4081 Synthetic oligonucleotide probe

4090 493

4091 agcagaatcc aacctgagta 21

4100 494

4101 20

4102 DNA

4103 Artificial Sequence

4110

4111 Synthetic oligonucleotide probe

4120 494

4121 gacgctatcc tctgtgctc 20

4130 495

4131 3283

4132 DNA

4133 Homo sapiens

4140 495

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 35 40 45
 His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro
 50 55 60
 Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn
 65 70 75
 His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His
 80 85 90
 Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu
 95 100 105
 Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro
 110 115 120
 Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp
 125 130 135
 Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu
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 Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys
 155 160 165
 Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly
 170 175 180
 Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile
 185 190 195

Gln Lys Asp Ala Phe Leu Asn Leu Thr	Lys Leu Lys Val Leu Ser
200	210
Leu Lys Asp Asn Asn Val Thr Ala Val	Pro Thr Val Leu Pro Ser
215	225
Thr Leu Thr Glu Leu Tyr Leu Tyr Asn	Asn Met Ile Ala Lys Ile
230	240
Thr Glu Asp Asp Phe Asn Asn Leu Asn	Gln Leu Gln Ile Leu Asp
245	255
Leu Ser Gly Asn Cys Pro Arg Cys Tyr	Asn Ala Pro Phe Pro Cys
260	270
Ala Pro Cys Lys Asn Asn Ser Pro Leu	Gln Ile Pro Val Asn Ala
275	285
Phe Asp Ala Leu Thr Glu Leu Lys Val	Leu Arg Leu His Ser Asn
290	300
Ser Leu Gln His Val Pro Pro Arg Trp	Phe Lys Asn Ile Asn Lys
305	315
Leu Gln Glu Leu Asp Leu Ser Gln Asn	Phe Leu Ala Lys Glu Ile
320	330
Gly Asp Ala Lys Phe Leu His Phe Leu	Pro Ser Leu Ile Gln Leu
335	345
Asp Leu Ser Phe Asn Phe Glu Leu Gln	Val Tyr Arg Ala Ser Met
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Asn Leu Ser Gln Ala Phe Ser Ser Leu	Lys Ser Leu Lys Ile Leu
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Arg Ile Arg Gly Tyr Val Phe Lys Glu	Leu Lys Ser Phe Asn Leu
380	390
Ser Pro Leu His Asn Leu Gln Asn Leu	Glu Val Leu Asp Leu Gly
395	405
Thr Asn Phe Ile Lys Ile Ala Asn Leu	Ser Met Phe Lys Gln Phe
410	420
Lys Arg Leu Lys Val Ile Asp Leu Ser	Val Asn Lys Ile Ser Pro
425	435
Ser Gly Asp Ser Ser Glu Val Gly Phe	Cys Ser Asn Ala Arg Thr
440	450
Ser Val Glu Ser Tyr Glu Pro Gln Val	Leu Glu Gln Leu His Tyr
455	465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser	Cys Arg Phe Lys Asn Lys
470	480

Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly	485	490	495
Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser	500	505	510
Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser	515	520	525
Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro	530	535	540
Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp	545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu Leu His Lys Leu Glu Val	560	565	570
Leu Asp Ile Ser Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile	575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys	590	595	600
Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr	605	610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His	620	625	629
Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu	635	640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn	650	655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro	665	670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe	680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp	695	700	705
Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn	710	715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile	725	730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg	740	745	750
Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr	755	760	765

Met Ile Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu	770	775	780
His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val	785	790	795
Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr	800	805	810
Arg Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val	815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu	830	835	840
Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val	845	850	855
Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile	860	865	870
Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile	875	880	885
Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys	890	895	900
Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys	905	910	915
Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu	920	925	930
Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln	935	940	945
Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys	950	955	960
Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His	965	970	975
Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe	980	985	990
Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys	995	1000	1005
Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln	1010	1015	1020
Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr	1025	1030	1035
Asp Asn His Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val	1040	1045	

411 497
4111 4199
4111 DNA
4118 Homo sapiens

400 497
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<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

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			20						25					30

Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
			35						40					45

Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
			50						55					60

Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
			65						70					75

Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
			80						85					90

Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
			95						100					105

Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
			110						115					120

Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
			125						130					135

Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
			140						145					150

Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
			155						160					165

Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
			170						175					180

Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
			185						190					195

Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
			200						205					210

Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
			215						220					225

Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
			230						235					240

Asp Phe Lys Gly Leu Ile Asn Leu Thr	Leu Leu Asp Leu Ser Gly	245	250	255
Asn Cys Pro Arg Cys Phe Asn Ala Pro	Phe Pro Cys Val Pro Cys	260	265	270
Asp Gly Gly Ala Ser Ile Asn Ile Asp	Arg Phe Ala Phe Gln Asn	275	280	285
Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser	Ser Thr Ser Leu Arg	290	295	300
Lys Ile Asn Ala Ala Trp Phe Lys Asn Met	Pro His Leu Lys Val	305	310	315
Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly	Glu Ile Val Ser Gly	320	325	330
Ala Phe Leu Thr Ile Leu Pro Arg Leu Glu	Ile Leu Asp Leu Ser	335	340	345
Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln	His Ile Asn Ile Ser	350	355	360
Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg	Ala Leu His Leu Arg	365	370	375
Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp	Asp Phe Gln Pro Leu	380	385	390
Met Gln Leu Pro Asn Leu Ser Thr Ile Asn	Leu Gly Ile Asn Phe	395	400	405
Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln	Asn Phe Ser Asn Leu	410	415	420
Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile	Ser Pro Leu Val Lys	425	430	435
Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser	Ser Phe Gln Arg His	440	445	450
Ile Arg Lys Arg Arg Ser Thr Asp Phe Glu	Phe Asp Pro His Ser	455	460	465
Asn Phe Tyr His Phe Thr Arg Pro Leu Ile	Lys Pro Gln Cys Ala	470	475	480
Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu	Asn Ser Ile Phe Phe	485	490	495
Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro	Asp Ile Ala Cys Leu	500	505	510
Asn Leu Ser Ala Asn Ser Asn Ala Gln Val	Leu Ser Gly Thr Glu	515	520	525

Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr	Asn Asn
530		535	540
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser	Asp
545		550	555
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg	Ile
560		565	570
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr	Asn
575		580	585
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu Thr	
590		595	600
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val	Phe
605		610	615
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn	Arg
620		625	630
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu	Asp
635		640	645
Leu Ser Leu Asn	Arg Leu Lys His Ile	Pro Asn Glu Ala Phe	Leu
650		655	660
Asn Leu Pro Ala	Ser Leu Thr Glu Leu	His Ile Asn Asp Asn	Met
665		670	675
Leu Lys Phe Phe	Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg	Leu
680		685	690
Glu Leu Leu Asp	Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr	Asp
695		700	705
Ser Leu Ser Asp	Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu	Ser
710		715	720
His Asn Arg Ile	Ser His Leu Pro Ser	Gly Phe Leu Ser Glu	Val
725		730	735
Ser Ser Leu Lys	His Leu Asp Leu Ser	Ser Asn Leu Leu Lys	Thr
740		745	750
Ile Asn Lys Ser	Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu	Ser
755		760	765
Met Leu Glu Leu	His Gly Asn Pro Phe	Glu Cys Thr Cys Asp	Ile
770		775	780
Gly Asp Phe Arg	Arg Trp Met Asp Glu	His Leu Asn Val Lys	Ile
785		790	795
Pro Arg Leu Val	Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln	Arg
800		805	810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp	815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr	830	835	840
Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp	845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr	860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser	875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu	890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu	905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp	920	925	930
Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val	935	940	945
Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe	950	955	960
Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile	965	970	975
Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu	980	985	990
Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro	995	1000	1005
Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn	1010	1015	1020
Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val	1025	1030	1035
Asp Ser Ile Lys Gln Tyr	1040		

<210> 499

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 409
cagatcca gctgtgaccg 20

<110> 500
<111> 20
<112> DNA
<113> Artificial Sequence

<210>
<211> Synthetic oligonucleotide probe

<400> 500
ctccatcagc ctctgatggg 20

<110> 501
<111> 45
<112> DNA
<113> Artificial Sequence

<210>
<211> Synthetic oligonucleotide probe

<400> 501
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<110> 502
<111> 71
<112> DNA
<113> Artificial Sequence

<210>
<211> Synthetic oligonucleotide probe

<400> 502
acccagacaa aaacgttctc c 21

<110> 503
<111> 34
<112> DNA
<113> Artificial Sequence

<210>
<211> Synthetic oligonucleotide probe

<400> 503
catccatggt ctcaccatt agcc 24

<110> 504
<111> 46
<112> DNA
<113> Artificial Sequence

<210>
<211> Synthetic oligonucleotide probe

<400> 504
ccgacaaact catgcagagc atcaaccaa gcaagaaaac agtatt 46

<210> 505
<211> 1738
<212> DNA
<213> Homo sapiens

<400> 505
ccagggtccaa ctgcacctcg gttctatcga ttgaattccc cggggatcct 50
ctagagatcc ctgcacctcg acccaacggt cgcacaagct ggccctgcac 100
ggctgcaagg gaggctcctg tggacaggcc aggcagggtg gctcaggag 150
gtgcctccag gcggccagtg ggctgaggc ccagcaagg gctagggtcc 200
atctccagtc ccaggacaca gcagcggcca ccatggccac gctgggctc 250
cagcagcatc agcagccccc aggacggggg aggcacaggt ggccccccac 300
accggagjga gacgtcctg cccctgtccg ggggatgaat gattctctc 350
cgccaggcca ccagaggag aagccacccc cgcctggagg cacaggccat 400
gaggggtctc caggaggtgc tgcctgatgtg gcttctgtg ttggcagtgg 450
gcggcacaga gcaagcctac cggcccggcc gtaggggtg tgcctgtccg 500
gtcacgggg accctgtctc cgagtccttc gtgcagcgtg tgtaccagcc 550
cttctcacc acctgagacg ggcacggggc ctgcagcacc taccgaacca 600
tctataggac cgcctacgc cgcagccctg ggcctggccc tgcaggcct 650
cgctacgcgt gctgcccggc ctggaagagg accagcgggc ttcctggggc 700
ctgtggagca gcaatatgc agccgcctat ccgjaacjga gggagctgtg 750
tcagccctgg ccgtgcgcgc tgcctgcag gatggcgggg tgacacttgc 800
cagtcagatg tggatgaatg cagtgcctag aggggcjgct gtcccagcg 850
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gtggccccca acccgacagg agtggacagt gcaatgaagj aagaagtga 1000
gaggtgcag tccaggjtg accctgtgga ggagaagctj cagctggtgc 1050
tgccccact gcacagcctg gctcgcagg cactggagca tgggctccg 1100
gacccggca gctcctggt gcactccttc cagcagctc gcgcctaga 1150
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cctgcaagaa agactcgtga ctgccagcg cccagcgtj gactgagccc 1250

ctcaagcgcg cctgcagccc ccacgcccct gcccaacatg ctggggggtcc 1300
 agaagccacc tcgggggtgac tgagcggaag gccaggcagg gccttccctcc 1350
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 ggctgggata ttctctgtja atccacccct ggctacccccc acctgggcta 1450
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 agctccctgc tggagcctjg gaccatggc acagggccagg cagccgggag 1550
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 aatgaaagct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
 aaaggggggc cggagctcta gactcgacct gcagaagctt ggcggccatg 1700
 gcccaacttg ttattgagc cttataatgg ttacaaat 1738

<110> 506
 <111> 273
 <112> PPT
 <113> Homo sapiens

<400> 506

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135
Ser	Asp	Val	Asp	Gln	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu

155	160	165
Gly His Ser Leu Ser Ala Asp Gly Thr Ieu Cys Val Pro Lys Gly		
170	175	180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala		
185	190	195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu		
200	205	210
Glu Glu Lys Leu Gln Leu Val Leu Ala Iro Leu His Ser Leu Ala		
215	220	225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu		
230	235	240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Gln		
245	250	255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys		
260	265	270
Lys Asp Ser		

0210: 507
 0211: 1700
 0212: DNA
 0213: Homo sapiens

0400: 507
 ggcaggcagg tgggctcag gaggtgcctc caggggcca gtgggctga 50
 ggcaccagca agggctaggg tccatctcca gtccaggac acagcagcg 100
 ccaccatggc cagcctggg ctccagcagc atcagagcag cccctgtggt 150
 tggcagcaaa gttcagcttg gctgggcccg ctgtgagggg cttagcgcta 200
 cggcctgcgg tgtcccgagg gctgaggtct cctcatcttc tccctagcag 250
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 gaggaacccc aaagccact ctgtagccag gatgagcagt gtgaatccag 350
 gcagccccca ggacggggga ggcacaggtg gcccccacca ccgggaggag 400
 cagctctctc cctgtctcgg gggatgactg attctctctc gccaggccac 450
 ccagaggaga aggcacccc gcctggaggc acaggccatg aggggctctc 500
 aggaggtgct gctgatgttg cttctggtgt tggcagtggg cggcacagag 550
 cagcctaac ggccggccg taggggtgtg gctgtccggg ctccgggga 600
 cctgtctctc gactgcttc tgcagcgtgt gtaccagccc ttctcacca 650

cctgagacgg gcaccgggcc tgcagcacct accgaaccat ctataggacc 700
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 tcccaaggcc aggtggcccc tcagctgagg gaaggtaaga gctccctgt 1600
 ggagcctggg acccatggca caggccaggc agcccgagg ctgggtgggg 1650
 cctcagtggg ggctgtgtgc tgacccccag cacaataaaa atgaaacgtg 1700

<E10> 508

<E11> 273

<E12> PRT

<E13> Homo sapiens

<F00> 508

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
1						5				10				15

Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
						20				25				30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
						35				40				45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135
Ser	Asp	Val	Asp	Gln	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	150
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Gln	155	160	165
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	170	175	180
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	185	190	195
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	200	205	210
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	215	220	225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	230	235	240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	245	250	255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	260	265	270

Lys Asp Ser

<E110> 509

<E111> 1538

<E112> DNA

<E113> Homo sapiens

<E100> 509

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ctgaggcccc agcaaggget aggttccatc tccagtccca ggacacagca 150
ggggccacca tggccacgac tgggtccag cagcatcaga agccccagg 200
accggggagg cacaggtggc ccccccacc cggaggagca gctcctggcc 250
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ccccggcga ggggtgtgtc tgtccgggtc cagggggacc ctgtctccga 450
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ccatggcaca ggccaggcag cccggaggct ggggtggggc tcagtggggg 1500

ctgctgctg acccccagca caataaaaat gaaacgtg 1538

<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60

Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75

Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90

Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105

Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120

Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135

Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150

Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu
				155					160					165

Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly
				170					175					180

Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala
				185					190					195

Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu
				200					205					210

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225

Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
260 265 270

Lys Asp Ser

<210> 511
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<300> 511
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<410> 512
<411> 22
<412> DNA
<413> Artificial Sequence

<420>
<421> Synthetic oligonucleotide probe

<400> 512
ttttccactc ctgtcgggtt gg 22

<210> 513
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 513
tggcgacatt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514
<211> 7690
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2039-2065
<223> unknown base

<400> 514
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<210> 515

<211> 364

<212> PRT

<213> Homo sapiens

<400> 515

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Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met

Met Ala Arg Gln Lys Gly Ile Phe Tyr Leu Thr Leu Phe Leu Ile	20	25	30
	35	40	45
Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu	50	55	60
Glu Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu	65	70	75
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp	80	85	90
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile	95	100	105
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln	110	115	120
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile	125	130	135
Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro	140	145	150
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe	155	160	165
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn	170	175	180
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr	185	190	195
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser	200	205	210
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr	215	220	225
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val	230	235	240
Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr	245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val	260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu	275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly	290	295	300
Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln			

	305	310	315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu			
	320	325	330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu			
	335	340	345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala			
	350	355	360
Glu Ala Glu Lys			

<210> 516
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> ensure
 <222> 35, 38, 88, 118, 135, 193, 213, 222
 <223> unknown base

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 agatttaggt attatagggg tggtaggggtt gatttttntt cctggaggct 100
 tttaggtttg gaactctcct ttctccacac gagencttcg accatcactg 150
 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200
 tcttcctcct ttntctctcc cncctcacaa tctatgtctt cgccttcaac 250
 tctgt 255

<310> 517
 <311> 24
 <312> DNA
 <313> Artificial Sequence

<320>
 <321> Synthetic oligonucleotide probe

<400> 517
 caacgtgatt tcaaagctgg gctc 24

<410> 518
 <411> 20
 <412> DNA
 <413> Artificial Sequence

<420>
 <421> Synthetic oligonucleotide probe

<400> 518

gcctcgatc aagaatttc 20

<210> 519

<211> 12

<212> RNA

<213> Artificial Sequence

<220>

<225> Synthetic oligonucleotide probe

<400> 519

agtgga gtc gacctcc 18

<210> 519

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<225> Synthetic oligonucleotide probe

<400> 519

ctaccgaa atctctcata gcc 24

<210> 511

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<225> Synthetic oligonucleotide probe

<400> 521

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<210> 512

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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agagcaaac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaa ccattcagcc 150

aaaaatgcac aattctatct cttgggcaat cttcaggggg ctggctgctc 200

tgtgtctctt ccaaggagtg ccggtgggca gaggagatgc caccttcccc 250

aaagctatgg acaacgtgac ggccgggcag ggggagagcg ccacctcag 300

gtgcactatt gacaacgggg tcaccggggt ggctggcta aacgcagca 350

ccatctcta tgctgggaat gacaagtggg gcctggatcc tcggtggtc 400

ctctctgagca acacccaaaac gcagtagagc atcgagatcc agaacgttga 450
 tgtgtatgac gagggccctt acacctgtct ggtgcagaca gacaaccacc 500
 aaaaagcttc tagggctcac ctcatctgtc aagtatctcc caaaattgta 550
 gagattttct cagatatctc cattaatgaa gggacaata ttagcctcac 600
 ctgcatagca actggttagac cagagcttac gggttacttg agacacatct 650
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 ggcacacccc gggagcagtc aggggaactac gagtgcagtg cctccaatga 750
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 catcatttcc agaagccaag ggtacagggtg tcccgtggg aaaaaaggg 850
 acactgcagt gtgaagcttc agcagtcacc taagcagaat tccagtgtta 900
 caaggatgac aaaagactga ttgaaggaaa gaaaggggtg aaagtggaaa 950
 acagaccttt cctctcaaaa ctcatcttcc tcaatgtctc tgaacatgac 1000
 catgggaact acacttggtt ggctccaac aagctggggc acaccaatgc 1050
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 ggcgcaccca ccaccaccca cacaacagca atggcaaac cgacagcaac 1250
 caatcagata tatacaaatg aaattagaag aaacacagcc tcatgggaca 1300
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 aaaaagaaat tgaatttgc ctgcagata tttaggtaca atggagtttt 1400
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 aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600
 gtgcacgtgc gggcactttg gtagactgtg ccaccaaggc gtgtgttgtg 1650
 aaacgtgaaa taaaagagc aaaaaaaaa 1679

<10> 523

<11> 344

<12> PRT

<13> Homo sapiens

<400> 523

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110	Phe	Thr	Gly	Leu	Ala	Ala	Leu	Cys	Leu	Phe	Gln	Gly	Val	Pro
			10						20					25
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val
			35						40					45
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp
			50						55					60
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu
			65						70					75
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu
			80						85					90
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val
			95						100					105
Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp
			110						115					120
Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser
			125						130					135
Pro	Lys	Ile	Val	Gln	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly
			140						145					150
Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro
			155						160					165
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val
			170						175					180
Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln
			185						190					195
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro
			200						205					210
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile
			215						220					225
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr
			230						235					240
Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp
			245						250					255
Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile	Glu	Gly	Lys	Lys	Gly	Val	Lys
			260						265					270
Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val
			275						280					285

Ser	Glu	His	Asp	Tyr	Gly	Asn	Tyr	Thr	Cys	Val	Ala	Ser	Asn	Lys
				290					295					300
Leu	Gly	His	Thr	Asn	Ala	Ser	Ile	Met	Leu	Phe	Gly	Pro	Gly	Ala
				305					310					315
Val	Ser	Glu	Val	Ser	Asn	Gly	Thr	Ser	Arg	Arg	Ala	Gly	Cys	Val
				320					325					330
Trp	Leu	Leu	Pro	Leu	Leu	Val	Leu	His	Leu	Leu	Leu	Lys	Phe	
				335					340					

<210> 524
 <211> 503
 <212> DNA
 <213> Homo sapiens

<400> 524
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 gag 505

<210> 525
 <211> 2602
 <212> DNA
 <213> Homo sapiens

<400> 525
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 tgaacgtcgc gctgcaggag ctgggagctg gcagcaacgt gggattccag 150
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 agcaggtgcc tctctactgc tggctgcact gcttctgggc tgccttggtg 250

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 cc 2602

<210> 526
 <211> 736
 <212> PRT
 <213> Homo sapiens

<400> 526
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 Phe Gln Lys Gly Thr Arg Gln Leu Leu Gly Ser Arg Thr Gln Leu
 20 25 30
 Glu Leu Val Leu Ala Gly Ala Ser Leu Leu Ala Ala Leu Leu
 35 40 45
 Leu Gly Cys Leu Val Ala Leu Gly Val Gln Tyr His Arg Asp Pro
 50 55 60

Ser	His	Ser	Thr	Cys	Leu	Thr	Glu	Ala	Cys	Ile	Arg	Val	Ala	Gly	65	70	75
Lys	Ile	Leu	Glu	Ser	Leu	Asp	Arg	Gly	Val	Ser	Pro	Cys	Glu	Asp	80	85	90
Phe	Tyr	Gln	Phe	Ser	Cys	Gly	Gly	Trp	Ile	Arg	Arg	Asn	Pro	Leu	95	100	105
Pro	Asp	Gly	Arg	Ser	Arg	Trp	Asn	Thr	Phe	Asn	Ser	Leu	Trp	Asp	110	115	120
Gln	Asn	Gln	Ala	Ile	Leu	Lys	His	Leu	Leu	Glu	Asn	Thr	Thr	Phe	125	130	135
Asn	Ser	Ser	Ser	Gln	Ala	Glu	Gln	Lys	Thr	Gln	Arg	Phe	Tyr	Leu	140	145	150
Ser	Cys	Leu	Gln	Val	Glu	Arg	Ile	Glu	Glu	Leu	Gly	Ala	Gln	Pro	155	160	165
Leu	Arg	Asp	Leu	Ile	Glu	Lys	Ile	Gly	Gly	Trp	Asn	Ile	Thr	Gly	170	175	180
Pro	Trp	Asp	Gln	Asp	Asn	Phe	Met	Glu	Val	Leu	Lys	Ala	Val	Ala	185	190	195
Gly	Thr	Tyr	Arg	Ala	Thr	Pro	Phe	Phe	Thr	Val	Tyr	Ile	Ser	Ala	200	205	210
Asp	Ser	Lys	Ser	Ser	Asn	Ser	Asn	Val	Ile	Gln	Val	Asp	Gln	Ser	215	220	225
Gly	Leu	Phe	Leu	Pro	Ser	Arg	Asp	Tyr	Tyr	Leu	Asn	Arg	Thr	Ala	230	235	240
Asn	Glu	Lys	Val	Leu	Thr	Ala	Tyr	Leu	Asp	Tyr	Met	Glu	Glu	Leu	245	250	255
Gly	Met	Leu	Leu	Gly	Gly	Arg	Pro	Thr	Ser	Thr	Arg	Glu	Gln	Met	260	265	270
Gln	Gln	Val	Leu	Glu	Leu	Glu	Ile	Gln	Leu	Ala	Asn	Ile	Thr	Val	275	280	285
Pro	Gln	Asp	Gln	Arg	Arg	Asp	Glu	Glu	Lys	Ile	Tyr	His	Lys	Met	290	295	300
Ser	Ile	Ser	Glu	Leu	Gln	Ala	Leu	Ala	Pro	Ser	Met	Asp	Trp	Leu	305	310	315
Glu	Phe	Leu	Ser	Phe	Leu	Leu	Ser	Pro	Leu	Glu	Leu	Ser	Asp	Ser	320	325	330
Glu	Pro	Val	Val	Val	Tyr	Gly	Met	Asp	Tyr	Leu	Gln	Gln	Val	Ser	335	340	345

Glu	Leu	Ile	Asn	Arg	Thr	Glu	Pro	Ser	Ile	Leu	Asn	Asn	Tyr	Leu	350	355	360
Ile	Trp	Asn	Leu	Val	Gln	Lys	Thr	Thr	Ser	Ser	Leu	Asp	Arg	Arg	365	370	375
Ile	Glu	Ser	Ala	Gln	Glu	Lys	Leu	Leu	Glu	Thr	Leu	Tyr	Gly	Thr	380	385	390
Lys	Lys	Ser	Cys	Val	Pro	Arg	Trp	Gln	Thr	Cys	Ile	Ser	Asn	Thr	395	400	405
Asp	Asp	Ala	Leu	Gly	Phe	Ala	Leu	Gly	Ser	Leu	Phe	Val	Lys	Ala	410	415	420
Thr	Phe	Asp	Arg	Gln	Ser	Lys	Glu	Ile	Ala	Glu	Gly	Met	Ile	Ser	425	430	435
Glu	Ile	Arg	Thr	Ala	Phe	Glu	Glu	Ala	Leu	Gly	Gln	Leu	Val	Trp	440	445	450
Met	Asp	Glu	Lys	Thr	Arg	Gln	Ala	Ala	Lys	Glu	Lys	Ala	Asp	Ala	455	460	465
Ile	Tyr	Asp	Met	Ile	Gly	Phe	Pro	Asp	Ile	Ile	Leu	Glu	Pro	Lys	470	475	480
Glu	Leu	Asp	Asp	Val	Tyr	Asp	Gly	Tyr	Glu	Ile	Ser	Glu	Asp	Ser	485	490	495
Phe	Phe	Gln	Asn	Met	Leu	Asn	Leu	Tyr	Asn	Phe	Ser	Ala	Lys	Val	500	505	510
Met	Ala	Asp	Gln	Leu	Arg	Lys	Pro	Pro	Ser	Arg	Asp	Gln	Trp	Ser	515	520	525
Met	Thr	Pro	Gln	Thr	Val	Asn	Ala	Tyr	Tyr	Leu	Pro	Thr	Lys	Asn	530	535	540
Glu	Ile	Val	Phe	Pro	Ala	Gly	Ile	Leu	Gln	Ala	Pro	Phe	Tyr	Ala	545	550	555
Arg	Asn	His	Pro	Lys	Ala	Leu	Asn	Phe	Gly	Gly	Ile	Gly	Val	Val	560	565	570
Met	Gly	His	Glu	Leu	Thr	His	Ala	Phe	Asp	Asp	Gln	Gly	Arg	Glu	575	580	585
Tyr	Asp	Lys	Glu	Gly	Asn	Leu	Arg	Pro	Trp	Trp	Gln	Asn	Glu	Ser	590	595	600
Leu	Ala	Ala	Phe	Arg	Asn	His	Thr	Ala	Cys	Met	Glu	Glu	Gln	Tyr	605	610	615
Asn	Gln	Tyr	Gln	Val	Asn	Gly	Glu	Arg	Leu	Asn	Gly	Arg	Gln	Thr	620	625	630

Leu Gly Glu Asn Ile Thr Asp Asn Gly Gly Leu Lys Ala Ala Tyr	635	640	645
Asn Ala Tyr Lys Ala Trp Leu Arg Lys His Gly Glu Glu Gln Gln	650	655	660
Leu Pro Ala Val Gly Leu Thr Asn His Gln Leu Phe Phe Val Gly	665	670	675
Phe Ala Gln Val Trp Cys Ser Val Arg Thr Pro Glu Ser Ser His	680	685	690
Glu Gly Leu Val Thr Asp Pro His Ser Pro Ala Arg Phe Arg Val	695	700	705
Leu Gly Thr Leu Ser Asn Ser Arg Asp Phe Leu Arg His Phe Gly	710	715	720
Cys Pro Val Gly Ser Pro Met Asn Pro Gly Gln Leu Cys Glu Val	725	730	735

Trp

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<223> Synthetic oligonucleotide probe

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gacctgaag gctcgggc t 21

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<212> DNA

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<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 567

<211> 25

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 567

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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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<210> 570

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 571

<211> 26

<212> DNA

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<210> 572

<211> 20

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<220>
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<400> 73
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<210> 74
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acttgagaca gaagtatgct gtcct 25

<210> 573

<211> 25

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<220>

<223> Synthetic oligonucleotide probe

<400> 573

ggttttgt tcaatcaccag cggctc 26

<210> 580

<211> 22

<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 580

tggaacagc tttttctggt aa 22

<210> 581

<211> 23

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<223> Synthetic oligonucleotide probe

<400> 581

gcaggaaacc ttccaatctg ag 22

<210> 582

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aaatattgct gacctcgccc a 21

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<20>
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<20>
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<10> 593
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<400> 595

taaggtacta atttgtgcta taacct 26

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gaactctgagt ctctgcttga 20

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<210> 598

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<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 509

atagcgatca ggtrattga 20

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<211> 22

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cttcctcacc acctgcgacg gg 22

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<212> DNA

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gpgtaggggt cctatagatg gtt 23

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<400> 605

gpgtgggat gaatgcagtg cta 23

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<211> 24

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atcaaacacg cgggcagtta ctgg 24

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<210> 611
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<213> Homo Sapien

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acccacccac caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaatc 200
ctgtggcgcg ccgcctgggt ccggggaaga ctgccagca ccaggggggtg 250
ggggagtgcg agctgaaagc tgcaggagag tgagcagccc tagcagggat 300
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 aaccttttgt ttttaaatg acctgccaag gtagctgaag accttttaga 2750
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 tgggacgttt gtcaaaaaaa aaaaaaaaaa aaaaaaaaaa 2840

<210> 612
 <211> 352
 <212> PRT
 <213> Homo Sapien

<400> 612
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 20 25 30
 Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn
 35 40 45
 Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu
 50 55 60
 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile
 65 70 75
 Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser
 80 85 90
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn
 95 100 105
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr

	110	115	120
Gln His Thr Pro Arg Thr Met Gln Val	His Leu Thr Val Gln Val		
125	130	135	
Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu			
140	145	150	
Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu			
155	160	165	
Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe			
170	175	180	
Gln Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln			
185	190	195	
Ala Gly Glu Tyr Gln Cys Ser Ala Glu Asn Ala Val Ser Phe Pro			
200	205	210	
Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile			
215	220	225	
Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu			
230	235	240	
Ile Arg Cys Glu Gly Ala Gly Val Pro Pro Pro Ala Phe Glu Trp			
245	250	255	
Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly Ile Ile			
260	265	270	
Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr Asn Val			
275	280	285	
Thr Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys			
290	295	300	
Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro Ser Thr			
305	310	315	
Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val Leu Phe Ser Cys			
320	325	330	
Trp Tyr Leu Val Leu Thr Leu Ser Ser Phe Thr Ser Ile Phe Tyr			
335	340	345	
Leu Lys Asn Ala Ile Leu Gln			
350			

<210> 613

<211> 1797

<212> DNA

<213> Homo Sapien

<400> 613

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 aaataanaa attctcaagg aggcacagct cttgagttag acccaacag 150
 ctgcttttca ccaatttca atggagcctt tcgaaatcaa tgttccaaag 200
 cccaagagga gaatggggt gaactttctc ctagctgtgg tggcatcta 250
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 ttgagaacac ctggctcagg gtgcattag gtgcaagtc ctgcagccc 450
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 aactcaact agaaccagg gatgttcaga atcaaagggt aacaaggcgc 550
 cccaggtctt caaggtcaca agggggcat gggcatgct ggtgcccctg 600
 ccccgccggg accactgct gagaaggag ccaaggggc tatgggacga 650
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 aactggaact cagggtgttc cgggcccctc tgggtgcagt ggacaccag 1050
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 aaaactcagt gtcgtcagg attgtcggca gtagtaacc aggcgggct 1400
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aattttgat gccattgtct tctgcgcgat gctgggttac tccaaaggaa 1500
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 ggtctgacc cggaaccct ttcacttctc tctctccgag gtgtctctgg 1700
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<210> 614

<211> 520

<212> PRT

<213> Homo Sapien

<400> 614

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Thr	Gln	Gln	Ala	Ala	Phe	His	Gln	Ile	Ala	Met	Glu	Pro	Phe	Gln
				20					25					30
Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser
				35					40					45
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala
				50					55					60
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg
				65					70					75
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp
				80					85					90
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His
				95					100					105
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu
				110					115					120
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp
				125					130					135
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln
				140					145					150
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro
				155					160					165
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys
				170					175					180
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln

185	190	195
Gly Pro Pro Gly Val Lys Gly Glu Ala	Gly Leu Gln Gly Pro Gln	
200	205	210
Gly Ala Pro Gly Lys Gln Gly Ala Thr	Gly Thr Pro Gly Pro Gln	
215	220	225
Gly Glu Lys Gly Ser Lys Gly Asp Gly	Gly Leu Ile Gly Pro Lys	
230	235	240
Gly Glu Thr Gly Thr Lys Gly Glu Lys	Gly Asp Leu Gly Leu Pro	
245	250	255
Gly Ser Lys Gly Asp Arg Gly Met Lys	Gly Asp Ala Gly Val Met	
260	265	270
Gly Pro Pro Gly Ala Gln Gly Ser Lys	Gly Asp Phe Gly Arg Pro	
275	280	285
Gly Pro Pro Gly Leu Ala Gly Phe Pro	Gly Ala Lys Gly Asp Gln	
290	295	300
Gly Gln Pro Gly Leu Gln Gly Val Pro	Gly Pro Pro Gly Ala Val	
305	310	315
Gly His Pro Gly Ala Lys Gly Glu Pro	Gly Ser Ala Gly Ser Pro	
320	325	330
Gly Arg Ala Gly Leu Pro Gly Ser Pro	Gly Ser Pro Gly Ala Thr	
335	340	345
Gly Leu Lys Gly Ser Lys Gly Asp Thr	Gly Leu Gln Gly Gln Gln	
350	355	360
Gly Arg Lys Gly Glu Ser Gly Val Pro	Gly Pro Ala Gly Val Lys	
365	370	375
Gly Glu Gln Gly Ser Pro Gly Leu Ala	Gly Pro Lys Gly Ala Pro	
380	385	390
Gly Gln Ala Gly Gln Lys Gly Asp Gln	Gly Val Lys Gly Ser Ser	
395	400	405
Gly Glu Gln Gly Val Lys Gly Glu Lys	Gly Glu Arg Gly Glu Asn	
410	415	420
Ser Val Ser Val Arg Ile Val Gly Ser	Ser Asn Arg Gly Arg Ala	
425	430	435
Glu Val Tyr Tyr Ser Gly Thr Trp Gly	Thr Ile Cys Asp Asp Glu	
440	445	450
Trp Gln Asn Ser Asp Ala Ile Val Phe	Cys Arg Met Leu Gly Tyr	
455	460	465
Ser Lys Gly Arg Ala Leu Tyr Lys Val	Gly Ala Gly Thr Gly Gln	

	470		475		480									
Ile	Trp	Leu	Asp	Asn	Val	Gln	Cys	Arg	Gly	Thr	Glu	Ser	Thr	Leu
	485								490					495
Trp	Ser	Cys	Thr	Lys	Asn	Ser	Trp	Gly	His	His	Asp	Cys	Ser	His
	500								505					510
His	Glu	Asp	Ala	Gly	Val	Glu	Cys	Ser	Val					
	515								520					

<210> 615
 <211> 647
 <212> DNA
 <213> Homo Sapien

<400> 615
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 aaaaacana atgaactga tggacttct ttaccactt gggttaactt 200
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 aagatactaa aagatcaca ctgtcacaac ctcccggaag gagtagctga 300
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 gttaacaag tagtaataaa agttaattca atctaaaaaa aaaaaaa 647

<210> 616
 <211> 33
 <212> PFT
 <213> Homo Sapien

<400> 616
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 20 25 30
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
 35 40 45

Ala	Asp	Leu	Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp
				50				55					60	
Arg	Gly	Lys	Gly	Cys	Gln	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Ser	Glu
				65				70					75	
Leu	Leu	Cys	Cys	Pro	Lys	Asp	Val	Phe	Phe	Gly	Pro	Lys	Ile	Ser
				80				85					90	
Phe	Val	Ile	Pro	Cys	Asn	Asn	Gln							
				95										

<210> 617
 <211> 2558
 <212> CNA
 <213> Homo Sapien

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 gggtcccggt aggcgcgctc tgcgcgcgcgc gagatgtgga atctccctca 200
 ccgaaaccgac tcggctgtgg ccacgcgcgc ccgcgcgcgc tggctgtgcg 250
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210 - 618

211 - 750

212 - PRT

21 - Homo Sapien

2400 - 618

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5 10 15

Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly
20 25 30

Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
35 40 45

Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
50 55 60

Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His
65 70 75

Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
80 85 90

Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu
95 100 105

Asp Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro
110 115 120

Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly
125 130 135

Asn Glu Ile Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro Gly
140 145 150

Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser
155 160 165

Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala
170 175 180

Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn
185 190 195

Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg
200 205 210

Gly Asn Lys Val	Lys Asn Ala Gln Leu	Ala Gly Ala Lys Gly Val
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Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr Phe	Ala Pro Gly Val Lys
230	235	240
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro	Gly Gly Gly Val Gln Arg
245	250	255
Gly Asn Ile Leu	Asn Leu Asn Gly Ala	Gly Asp Pro Leu Thr Pro
260	265	270
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr	Arg Arg Gly Ile Ala Glu
275	280	285
Ala Val Gly Leu	Pro Ser Ile Pro Val	His Pro Ile Gly Tyr Tyr
290	295	300
Asp Ala Gln Lys	Leu Leu Glu Lys Met	Gly Gly Ser Ala Pro Pro
305	310	315
Asp Ser Ser Trp	Arg Gly Ser Leu Lys Val	Pro Tyr Asn Val Gly
320	325	330
Pro Gly Phe Thr	Gly Asn Phe Ser Thr	Gln Lys Val Lys Met His
335	340	345
Ile His Ser Thr	Asn Glu Val Thr Arg	Ile Tyr Asn Val Ile Gly
350	355	360
Thr Leu Arg Gly	Ala Val Glu Pro Asp	Arg Tyr Val Ile Leu Gly
365	370	375
Gly His Arg Asp	Ser Trp Val Phe Gly	Gly Ile Asp Pro Gln Ser
380	385	390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr Leu
395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala Ser
410	415	420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp Ala
425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr Ile
440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val Asp
455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys Glu
470	475	480
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr Glu
485	490	495

Ser	Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro
				500					505					510
Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe
				515					520					525
Gln	Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn
				530					535					540
Trp	Glu	Thr	Asn	Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val
				545					550					555
Tyr	Glu	Thr	Tyr	Glu	Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe
				560					565					570
Lys	Tyr	His	Leu	Thr	Val	Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe
				575					580					585
Glu	Leu	Ala	Asn	Ser	Ile	Val	Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr
				590					595					600
Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala	Asp	Lys	Ile	Tyr	Ser	Ile	Ser
				605					610					615
Met	Lys	His	Pro	Gln	Glu	Met	Lys	Thr	Tyr	Ser	Val	Ser	Phe	Asp
				620					625					630
Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn	Phe	Thr	Glu	Ile	Ala	Ser	Lys
				635					640					645
Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe	Asp	Lys	Ser	Asn	Pro	Ile	Val
				650					655					660
Leu	Arg	Met	Met	Asn	Asp	Gln	Leu	Met	Phe	Leu	Glu	Arg	Ala	Phe
				665					670					675
Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val
				680					685					690
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe
				695					700					705
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp
				710					715					720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala
				725					730					735
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<111> 50

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<113> Artificial Sequence

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<223> Synthetic Oligonucleotide probe

<400> 624

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